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| 70 | It. | Walv |

riale, mary

Uim, John

From: Sent:

Wednesday, October 22, 2003 3:36 PM

To:

Hale, Mary

Subject:

RE: problem with search request for SN 09/851,494

OK, let's modify the search. I need a search of nucleotides 5500 to 7000 and 9000 to 9200 of SEQ ID NO:1, which contain specifically claimed diagnostic mutations outside of a coding region, as well as nucleotides 400 to 1500 of SEQ ID NO:2, which appears to be a coding region within SEQ ID NO:1 and which contains seven additional diagnostic mutations. If this presents a problem, I can divide SEQ ID NO:2 into fragments containing the specifically recited mutations.

----Original Message----

From: Hale, Mary

Sent: Tuesday, October 21, 2003 3:46 PM

To: Ulm, John

Cc: Martinell, James

Subject: RE: problem with search request for SN 09/851,494

Importance: High

per attached note

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| STAFF USE ONLY | Type of Search | Vendors and cost where applicable |
| Searcher: | NA Sequence (#) | STN |
| Searcher Phone #: | AA Sequence (#) | Dialog |
| Searcher Location: | Structure (#) | Questel/Orbit |
| Date Searcher Picked Up: | Bibliographic | Dr.Link |
| Date Completed. | Litigation | |
| Searcher Prep & Review Time: | Fulltext | |
| Clencal Prep Time: | Patent Family | www/internet |
| Online Time: | Other | Other (specify) |

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October 27, 2003, 18:04:00 ; Search time 441 Seconds (without alignments) 220.243 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                               1 MTAPAGPRGSETERLLTPNP......CSLLCCCGRDPSEEHSLLVN 580
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         629382 segs, 167460630 residues
                                                                                                                    OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                   Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                         US-09-851-494B-3
                                                                                                                                                                                                                                                                                                                                                                                                        BLOSUM62
                                                                                                                                                                                                                                                                                                                    Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                        Scoring table:
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Sequence:

Title:

Run on:

Searched:

Maximum Match 100% Listing first 45 summaries Database :

Post-processing: Minimum Match 0%

| Cgn2_6/ptcdata/1/pubpaa/US09B_PUBCOMB.pep: | Cgn2_6/ptcdata/1/pubpaa/US09E_PUBCOMB.pep: | Cgn2_6/ptcdata/1/pubpaa/US09E_NEW_PUB.pep: | Cgn2_6/ptcdata/1/pubpaa/US10A_PUBCOMB.pep: | Cgn2_6/ptcdata/1/pubpaa/US10B_PUBCOMB.pep: | Cgn2_6/ptcdata/1/pubpaa/US10E_PUBCOMB.pep: | Cgn2_6/ptcdata/1/pubpaa/US10E_NEW_PUB.pep: | Cgn2_6/ptcdata/1/pubpaa/US10E_NEW_PUB.pep: | Cgn2_6/ptcdata/1/pubpaa/US60_NEW_PUB.pep: | Cgn2_6/ptcdata/1/pubpaa/US60_NEW_PUB.pep: Published Applications AA:*

(cgn2_6/ptcdata/1/pubpaa/USO7_PUBCOMB.pep:*

(cgn2_6/ptcdata/1/pubpaa/PCT_NEW_PUB.pep:*

(cgn2_6/ptcdata/1/pubpaa/USO6_NEW_PUB.pep:*

(cgn2_6/ptcdata/1/pubpaa/USO6_PUBGOMB.pep:*

(cgn2_6/ptcdata/1/pubpaa/USO7_NEW_PUB.pep:*

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(cgn2_6/ptcdata/1/pubpaa/PCTUS_PUBGOMB.pep:*

(cgn2_6/ptcdata/1/pubpaa/USO8_NEW_PUB.pep:*

(cgn2_6/ptcdata/1/pubpaa/USO8_NEW_PUB.pep:* 6/ptodata/1/pubpaa/US09A PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| | Description | Sequence 2, Appli | Sequence 13, Appl | Sequence 13, Appl | Sequence 2, Appli | Sequence 63, Appl | · o | 28. 7 | 24. 7 | Sequence 22, Appl | 713, | 162, 7 | Sequence 45089, A | Sequence 2, Appli | Sequence 6, Appli | |
|-----------|----------------|-------------------|-------------------|-------------------|-------------------|-------------------|------------------|------------------|------------------|-------------------|--------------------|-------------------|---------------------|-------------------|-------------------|---------------------|
| SUMMARIES | ID | US-09-828-466-2 | US-09-965-529-13 | 48-09-969-680A-13 | US-10-103-458-2 | US-09-820-893-63 | US-10-114-153-26 | US-10-114-153-28 | US-10-114-153-24 | US-10-114-153-22 | US-09-866-050A-713 | US-09-796-753-162 | US-09-864-761-45089 | US-10-005-211-2 | US-09-828-466-6 | US-09-864-761-41295 |
| | DB | 6 | 10 | 11 | 14 | σ | 12 | 13 | 12 | 12 | 11 | 11 | σ | 1.4 | σ | Ø |
| | Length DB | 580 | 580 | 580 | 580 | 511 | 538 | 266 | 544 | 540 | 255 | 193 | 69 | 621 | 996 | 16 |
| οlo | Query Match | 100.0 | 100.0 | 100.0 | 100.0 | 86.9 | 44.9 | 44.6 | 44.6 | 42.8 | 40.0 | 22.5 | 9.3 | 5.0 | 5.0 | 4.9 |
| | Score | 3067 | 3067 | 3067 | 3067 | 2665 | 1376 | 1368 | 1367 | 1314 | 1226 | 689 | 281.5 | 152.5 | 152.5 | 150.5 |
| | Result No. | Н | 2 | m | 4 | ιΩ | v | 7 | ထ | σv | 10 | 11 | 12 | 13 | 14 | 15 |

| Sequence 48727, A | 33 | ì | Sequence 44873, A | ۲, | 'n | | 46 | Sequence 2, Appli | 12 | 25 | Seguence 524, App | equence 52 | 52 | equence 52. | 25 | 25 | equence 52 | equence 52 | 52 | 52 | equence 52 | equence 52 | Seguence 524, App | 52 | e 52 | e 52 | Sequence 524, App | e 52 | e 52 |
|-------------------|------------|----------------|-------------------|---------------|-----------------|------------------|------------------|-------------------|-----------------|------------------|-------------------|-----------------|-----------------|-----------------|-----------------|-----------------|------------------|-----------------|----------------------|------------------|-----------------|------------------|-------------------|-----------------|-----------------|-----------------|-------------------|----------|-----------------|
| -761-4872 | 2 US-10-02 | US-09-753-008- | US-09-864-7 | US-09-753-008 | US-09-796-720B- | 2 US-10-146-733- | US-09-864-761-44 | 0 US-09-808-571A- | US-10-288-160-1 | US-10-199-672-52 | US-10-187-749- | US-10-194-457-5 | US-10-184-642-5 | US-10-196-747-5 | US-10-173-689-5 | US-10-173-690-5 | US-10-173-691-52 | US-10-173-692-5 | .2 US-10-173-694-524 | US-10-173-698-52 | US-10-173-699-5 | US-10-173-707-52 | US-10-174-569-5 | US-10-174-583-5 | US-10-174-587-5 | US-10-174-589-5 | US-10-174-591-5 | US-10-17 | US-10-175-742-5 |
| 224 9 | σ, | 866 | m | 89 | 724 1 | 24 | 49 | 447 | 323 1 | 1 989 | 686 1 | 686 1 | 686 1 | 686 1 | 686 1 | 686 1 | 686 1 | 686 1 | 686 1 | 686 1 | 686 1 | 686 1 | 686 1 | 686 1 | 686 1 | 686 1 | 686 1 | 686 1 | 686 1 |
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| 41. | 139.5 | ω | a | a | 2 | N | 113 | 106.5 | 101 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 |
| 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | <u>გ</u> | 40 | 41 | 42 | 43 | 44 | 45 |

ALIGNMENTS

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61 RKPCKLMLQVVKILVVTVQLILFGLSNQLAVTFREENTIAFRHLFLLGYSDGADDTFAAY 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 3067; DB 9; Length 580; 100.0%; Pred. No. 2.4e-289; ative 0; Mismatches 0; Indels 0;
RESULT 1
US-09-828-466-2
| Sequence 2, Application US/09828466
| Sequence 2, Application US/09828466
| Sequence 2, Application US/09828466
| Sequence 3, Application US/09828466
| Sequence 4, Application US/09/828466
| APPLICANT: Curtis, RNY A.J.
| APPLICANT: Silos-Sautiago, Immaculada
| TILLE OF INVENTION: 54420, A NOVEL HUMAN CALCIUM CHANNEL
| FILLE REFERENCE: MNI-125CP
| CURRENT APPLICATION NUMBER: US/09/828,466
| CURRENT PILING DATE: 2001-04-06
| PRIOR PILING DATE: 2000-04-07
| NUMBER OF SEQ ID NOS: 7
| SOFTWARE: Patentin Ver. 2.0
| SEQ ID NO. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 580; Conservative
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Best Local Similarity
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                                                                                     301 PDVVVILTCSLSFLLCARSLIRGFLLQNEFVGFMWRQRGRVISLWERLEFVNGWYILLVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc feature; OTHER INFORMATION: Incyte ID No. US20030124649A1 977658CD1
US-09-969-680A-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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100.0%; Pred. No. 2.4e-289;
Live 0; Mismatches 0; 1
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APPLICANT: LAL, Preet; YUE, Henry
APPLICANT: LAL, Preet; YUE, Henry
APPLICANT: BURGORD, Nei; AZIMZAI, Yalda
APPLICANT: BURGORD, Nei; AZIMZAI, Yalda
APPLICANT: BATGEN, Mariah R.; LU, Dyung Aina M.
APPLICANT: PATTERSON, Chandra
TITLE OF INVENTION: MEMBRANE ASSOCIATED PROTEINS
TITLE OF INVENTION: MEMBRANE ASSOCIATED PROTEINS
CURRENT APPLICATION NUMBER: US/09/969,680A
CURRENT FILING DATE: 2001-10-02
PRIOR FILING DATE: 1999-08-17
PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/149,641
PRIOR APPLICATION NUMBER: 60/149,641
PRIOR APPLICATION NUMBER: 60/149,641
PRIOR PILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 13, Application US/09969680A Publication No. US20030124649A1
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TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
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                                                                                              481 QAQQGRSSLVWLFSQLYLYSFISLFIYMVLSLFIALITGAYDTIKHPGGAGAEBSELQAY
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                                                                    NLQSLINNEIPDCYTFSVLITFDNKAHSGRIPISLETQAHIQECKHPSVFQHGDNSFRLL
                                                                                                                                                     FDVVVILTCSLSFLLCARSLLRGFLLQNEFVGFMWRQRGRVISLWERLEFVNGWYILLVT
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APPLICANT: YUE, Henry
APPLICANT: BANDAN, Olga
APPLICANT: BURFORD, Neil
APPLICANT: AZIMZAI, Yalda
APPLICANT: AZIMZAI, Yalda
APPLICANT: AZIMZAI, Yalda
APPLICANT: BAUGHW, Mariah R.
APPLICANT: PATTERSON, CHandra
APPLICANT: PATTERSON, CHANGRA SSOCIATED PROTEINS
FILE REFERENCE: PF-0731 USA
CURRENT APPLICATION NUMBER: US/09/965,529
CURRENT PILING DATE: 1999-08-16
PRIOR APPLICATION NUMBER: 60/149,641; 60/164,203; PCT/US00/22315
PRIOR FILING DATE: 1999-08-17; 1999-11-09; 2000-08-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020182671A1 977658CD1
US-09-965-529-13
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Publication No. US20020182671A1
GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 580; Conservative
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ORGANISM: Homo sapiens
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; COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-820-893-63
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                                                                                                                                                            301 FDVVVILTCSLSFLLCARSLLRGFLLQNEFVGFMWRQRGRVISLWERLEFVNGWYILLVT
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Pred. No. 2.5e-250;
1; Mismatches 3;
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Patent No. US20020076705A1
GENERAL INFORMATION
TITLE OF INVENTION: 31 Human Secreted Proteins
FILE REFERENCE: PS039F1
CURRENT APPLICATION NUMBER: US/09/820,893
CURRENT FILING DATE: 2001-03-30
PRIOR PILING DATE: 2000-03-20
PRIOR APPLICATION NUMBER: 69/531,119
PRIOR FILING DATE: 1998-10-02
PRIOR FILING DATE: 1998-10-02
NUMBER OF SEQ ID NOS: 140
SOFTWARE: PatentIn Ver: 2.0
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Best Local Similarity 99.2%
Matches 507, Conservative
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ORGANISM: Homo sapiens
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NAME/KEY: SITE
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US-09-820-893-63
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US-10.103-458-2
| Sequence 2, Application US/101003458
| Publication No. US2020197680A1
| GENERAL INFORMATION:
| APPLICANT: Curtis, ROTY A.J.
| TITLE OF INVERTION: 54420, A NOVEL HUMAN CALCIUM CHANNEL
| FILE REFERENCE: MNI-125
| CURRENT APPLICATION NUMBER: US/10/103,458
| CURRENT APPLICATION NUMBER: US/09/544,797
| PRIOR APPLICATION NUMBER: US/09/544,797
| NUMBER OF SEQ ID NOS: 3
| SEQ 
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100.0%; Pred. No. 2.4e-289;
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TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                97 NTIAFRHLFLLGYSDGADDTF--AAYTREQLYQAIFHAVDQYLALPDVSLGRYAYVRGGG
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                                                                                                                                                                                                                                            Length 538;
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       PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/283678
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/284234
PRIOR FILING DATE: 2001-04-17
                                                                                                                                                                                                                                        ; Sequence 28, Application US/10114153; Publication No. US20030185815A1; GENERAL INFORMATION:
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APPLICANT: Shenoy, Surseh
APPLICANT: Kekuda, Ramesh
APPLICANT: Rastelli, Luca
APPLICANT: Mezes, Peter
APPLICANT: Smithson, Glennda
APPLICANT: Gmithson, Glennda
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Guo, Xiaojia
Gerlach, Valerie
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Boldog, Ferenc
                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
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Best Local S
Matches 268
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TITLE OF INVENTION: ENCODING THE ANTIGENS, AND METHODS OF USE
FILE SPERENCE: 21402-322A
FILE OF INVENTION: ENCODING THE ANTIGENS, AND METHODS OF USE
CURRENT APPLICATION NUMBER: 05/281086
PRIOR APPLICATION NUMBER: 60/281086
PRIOR PALING DATE: 2001-04-05
PRIOR PLING DATE: 2001-04-05
PRIOR PLING DATE: 2001-04-06
PRIOR PLING DATE: 2001-04-10
PRIOR PLING DATE: 2001-04-12
429
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                                                        IMKIGIBAKNLASYDVCSILLGTSTLLVWVGVIRYLTFFHNYNILIATLRVALPSVMRFC
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Heyes, Melvyn
U, Jingfang
Peyman, John
Catterton, Elina
MacDougall, John
Edinger, Shlomit
Stone, David
Mazur, Ann
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Publication No. US20030185815A1
GENERAL INFORMATION:
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APPLICATION NUMBER: 60/283657
FILING DATE: 2001-04-13
APPLICATION NUMBER: 60/283710
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APPLICANT: Shenoy, Suresh
APPLICANT: Kekuda, Ramesh
APPLICANT: Rastelli, Luca
APPLICANT: Mezes, Peter
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Gangolli, Esha
Vernet, Corine
Spytek, Kimberly
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Gerlach, Valerie
Casman, Stacie
Boldog, Ferenc
Li, Li
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Miller, Charles
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TITLE OF INVENTION: NOVEL ANTIBODIES THAT BIND TO ANTIGENIC POLYPEPTIDES, NUCLEIC ACTITLE OF INVENTION: ENCODING THE ANTIGENS, AND METHODS OF USE
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                                                                                                                                                                                                                                                                          453 KPRSLSMVSECLFSLINGDDMFVTFAAMQAQQGRSSLVWLFSQLYLYSFISLFIYMVLSL 512
                                                                                                                                                                                                                                                                                                                513 FIALITGAYDTIKHPGGAGABESELQAYIAQCQDSPTSGKFRRGSGSACSLLCCCGRDPS 572
                                                                                                                                                                                                                                                                                                                                                                                                                                            502 FIALITOSYDTIKKFQQNGFPETDLQEFLKECS---SKEEYQKESSAFLSCICCRRRKRS 558
                                                         333 FMWRQRGRVISLWERLEFVNGWYILLVTSDVLFISGTIMKIGIEAKNLASYDVCSILLGT 392
                                                                                    325 FFLEKYKRPVCDTDQWEFINGWYVLVIISDLMTIIGSILKMEIKAKNLTNYDLCSIFLGT 384
265 FDSDAKIBECKDINIFGSAQKNAQYVLVFDAFVIVICLASLILCTRSIVLALRIRKRFLN 324
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CURRENT APPLICATION NUMBER: US/10/114,153
CURRENT FILING DATE: 2002-08-06
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PRIOR FILING DATE: 2001-04-03
PRIOR PILING DATE: 2001-04-03
PRIOR FILING DATE: 2001-04-05
PRIOR FILING DATE: 2001-04-05
PRIOR PILING DATE: 2001-04-06
PRIOR PILING DATE: 2001-04-06
PRIOR PILING DATE: 2001-04-10
PRIOR PILING DATE: 2001-04-11
PRIOR PILING DATE: 2001-04-12
PRIOR PILING DATE: 2001-04-12
PRIOR PILING DATE: 2001-04-12
PRIOR PILING DATE: 2001-04-12
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Heyes, Melvyn
Ju, Jingfang
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APPLICANT: Shenoy, Suresh
APPLICANT: Kekuda, Ramesh
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Zerhusen, Bryan
Tchernev, Velizar
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Catterton, Elina
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Edinger, Shlomit
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Spytek, Kimberly
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Gerlach, Valerie
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TITLE OF INVENTION: NOVEL ANTIBODIES THAT BIND TO ANTIGENIC POLYFEPTIDES, NUCLEIC ACT
TITLE OF INVENTION: HOVEL ANTIBODIES THAT BIND TO ANTIGENIC POLYFEPTIDES, NUCLEIC ACT
TITLE OF INVENTION: NOVEL ANTIBENS, AND METHODS OF USE
FILE REFERENCE: 21402-322A
CURRENT APPLICATION NUMBER: 40/28106
PRIOR FILING DATE: 2001-04-05
PRIOR PRILING DATE: 2001-04-05
PRIOR PELICATION NUMBER: 60/28230
PRIOR FILING DATE: 2001-04-06
PRIOR FILING DATE: 2001-04-06
PRIOR FILING DATE: 2001-04-10
PRIOR PELING DATE: 2001-04-12
PRIOR PELING DATE: 2001-04-12
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PRIOR PELING DATE: 2001-04-13
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                                                               Tchernev, Velizar
Gangolli, Esha
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Patturajan, Meera
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MacDougall, John
Edinger, Shlomit
Stone, David
Mazur, Ann
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Spytek, Kimberly
                               Zerhusen, Bryan
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CORGANISM: Homo sapiens
US-10-114-153-28
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Best Local S:
Matches 267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          306 ILTCSLSFLLCARSLLRGFLLQ-----NEFVGFMWRQRGRVISLWERLEFVNGWYILLVT 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           282 IASCEVIFCI----FLFVFILGELRKVNEFKSAYFR-----SVWNWLE-----MLLLL 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57
                                                                                                                                                                                                                                                                                                                                                                                                                                                       454 FRSLSMVSECLFSLINGDDMFVTFAAMQAQQGRSSLVWLFSQLYLYSFISLFIYMVLSLF
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                                                                                                                                                                                                               5.00e-28
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Publication No. US20020194636A1
GENERAL INFORMATION:
TITLE OF INVENTION: TRANSCENIC MICE CONTAINING
TITLE OF INVENTION: POLYCYSTIN RELATED GENE DISRUPTIONS
FILE REPERENCE: R-225
CURRENT APPLICATION NUMBER: US/10/005,211
CURRENT PILING DATE: 2001-12-04
PRIOR PILING DATE: 2000-12-13
PRIOR PILING DATE: 2000-12-13
PRIOR PILING DATE: 2000-12-13
PRIOR PILING DATE: 2000-12-04
NUMBER OF SEQ ID NOS: 4
NUMBER OF SEQ ID NOS: 4
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                                      PEATURE:
CHEMICANIEN: Homo sapiens
CHEMICANIEN: PRORMATION: MAP TO ACO13291.4
CTHEMINFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.5
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.5
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.46
OTHER INFORMATION: STREAM HIT: NA1861.1, EVALUE 5.00e-2
US-09-864-761-45089
                                                                                                                                                                                                                                                                                                                        Length
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21.5%; Pred. No. 9.6e-06;
"...marches 98;
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Pred. No. 1.1e-19;
                                                                                                                                                                                                                                                                                                                                                                    6; Mismatches
                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 79.2%;
Matches 57; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Mus musculus
US-10-005-211-2
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Best Local Similarity
Matches 52; Conserv
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VK 498
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Patent No. US20020048763A1

GENERAL INFORMATION:

APPLICANT: Penn, Sharron G.

APPLICANT: Pann, David K.

APPLICANT: Hancel, David K.

APPLICANT: Chen, Wensheng

TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

FILE PEFERENCE: Acountica-X-1

CURRENT APPLICATION NUMBER: US/09/864,761
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                                                       299 LLFDVVVILTCSLSFLLCARSLLRGFLLQNEFVGFMWRQRGRVISLWERLEFVNGWYILL 358
                                                                                                                                                                                              62 IISDILTIIGSILKWEIQAKSLTSYDVCSILLGTSTMLVWLGVIRYLGFFAKYNLLILT 121
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                                                                                        359 VISDVLTISGTIMKIGIBAKNLASYDVCSILLGTSTLLVWVGVIRYLTFFHNYNILIATL
                                                                                                                                                                                                                                                                      419 RVALPSVMRFCCCVAVIYLGYCFCGWIVLGPYHVKFRSLSWVSECLFSLINGDDMFVTFA
                Gaps
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             31; Indels
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PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-05-26
PRIOR PELING DATE: 2000-05-26
PRIOR PELING DATE: 2000-05-26
PRIOR PELING DATE: 2000-08-03
PRIOR PELING DATE: 2000-08-03
PRIOR PELING DATE: 2000-10-04
PRIOR PELING DATE: 2000-10-04
PRIOR PILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-10-30
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR PILING DATE: 2001-01-30

        31; Mismatches
        Conservative
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Matches 124;
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FEATURE:
OTHER INFORMATION: MAP TO ACO13291.4
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.4
OTHER INFORMATION: EXPRESSED IN PETAL LIVER, SIGNAL = 2.1
OTHER INFORMATION: EXPRESSED IN PETAL LIVER, SIGNAL = 2.2
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.2
OTHER INFORMATION: EXPRESSED IN HORT LIVER, SIGNAL = 2.2
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.2
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.1
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.2
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.2
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.2
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SOFTWARE: Annomax Sequence Listing Engine vers: 1.1
SLENGTH: 76
   PRIOR APPLICATION NUMBER: PCT/USO1/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR PLILNG DATE: 2001-01-30
PRIOR PLILNG DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00668
PRIOR APPLICATION NUMBER: PCT/USO1/00663
PRIOR APPLICATION NUMBER: PCT/USO1/00663
PRIOR APPLICATION NUMBER: PCT/USO1/00662
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR PLILNG DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR PLILNG DATE: 2001-01-30
PRIOR PLILNG DATE: 2000-09-21
PRIOR PLING DATE: 2000-09-21
PRIOR PLING DATE: 2000-09-21
PRIOR PLING DATE: 2000-09-30
PRIOR PLING DATE: 2000-09-30
PRIOR PLING DATE: 2000-09-30
PRIOR PLING DATE: 2000-09-30
PRIOR PLING DATE: 2001-01-29
PRIOR PLING DATE: 2001-01-29
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Job time : 446 secs
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Matches 28; Conserv
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APPLICANT: Penn, Sharron G.
APPLICANT: Hank, David K.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         350 FVNGWYILLVTSDVLTISGTIMKIGIEAKNLASYDVCSILLGTSTLLVWVGVIRYLTFFH 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               410 NYNILIATLRVALPSVMRFCCCVAVIYLGYCFCGWIVLGPYHVKFRSLSMVSECLFS--- 466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            548 HVAYWQ--------IQFNNISAVMV-----------FLVWIKLFKFINFNR 579
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 966;
                   Sequence 6, Application US/09828466
; Patent No. US20020035056A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.;
APPLICANT: Silos-Santiago, Immaculada
; TITLE OF INVENTION: 54420, A NOVEL HUMAN CALCIUM CHANNEL
; TITLE OF INVENTION: 54420, A NOVEL HUMAN CALCIUM CHANNEL
; CURRENT APPLICATION NUMBER: US/09/828,466
; CURRENT APLIANG DATE: 2001-04-06
; PRIOR PILIANG DATE: 2001-04-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 6
; SEQ ID NO 6
; LENGTH: 966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 5.0%; Score 152.5; DB 9; Length Best Local Similarity 21.3%; Pred. No. 1.8e-05; Matches 59; Conservative 49; Mismatches 104; Indels
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR PEPLICATION NUMBER: US 60/180,312
PRIOR PELLING DATE: 2000-02-04
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 032,366
PRIOR APPLICATION NUMBER: US 032,366
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR PLING DATE: 2000-10-04
PRIOR PLING DATE: 2000-09-27
PRIOR PLING DATE: 2000-09-27
PRIOR PLING DATE: 2001-01-30
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Patent No. US20020048763A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
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US-09-828-466-6
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October 27, 2003, 17:43:58; Search time 90 Seconds (without alignments) 1663.006 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                     830525 seqs, 258052604 residues
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sp_bacteria:*
sp_fungl:*
sp_human:*
sp_invertebrate:*
sp_mammal:*
sp_organelle:*
sp_phage:*
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Maximum DB seg length: 200000000
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Perfect score:
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                                                                                                                                                                                                                                      Sequence:
                                                                                                                   Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result So.

| | Description | Q9gzul homo sapien | Q9h4b3 homo sapien | Q9h292 homo sapien | Q99j21 mus musculu | Q9h4b5 homo sapien | Q8bs73 mus musculu | Q8r4f0 mus musculu | Q8bsg1 mus musculu | Q8cdb2 mus musculu | Q8tdd5 homo sapien | Q9nv09 homo sapien | Q8izk6 homo sapien | Q9cqd3 mus musculu | Q8k595 mus musculu | Q8k2t6 mus musculu | Q9vw35 drosophila |
|-----|-----------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|
| | QI | Q9GZU1 | Q9H4B3 | Q9H292 | 099721 | Q9H4B5 | Q8BS73 | QSR4F0 | Q8BSG1 | Q8CDB2 | QRIDDS | 60VV6Q | Q81ZK6 | Q9CQD3 | Q8K595 | Q8K2T6 | Q9VW35 |
| | DB | 4 | 4 | 4 | 11 | 4 | 11 | H | 금 | H | 4 | 4 | 4 | 11 | Ξ | 11 | n |
| | Match Length DB | 580 | 280 | 581 | 580 | 545 | 594 | 553 | 591 | 593 | 553 | 497 | 538 | 538 | 995 | 538 | 652 |
| * č | Match | 100.0 | 7.66 | 94.0 | 91.9 | 9.09 | 53.1 | 53.0 | 53.0 | 52.9 | 52.9 | 45.5 | 44.8 | 43.5 | 43.5 | 43.4 | 33.4 |
| | Score | 3067 | 3059 | 2884.5 | 2820 | 1859.5 | 1628.5 | 1626.5 | 1626.5 | 1623.5 | 1621 | 1396 | 1374 | 1335 | 1335 | 1332 | 1025.5 |

| Q81877 caenorhabdi Q81878 caenorhabdi Q8156 caenorhabdi Q805156 caenorhabdi Q8072 caenorhabdi Q8073 homo sapien Q90453 homo sapien Q80729 mus musculu Q80729 mus musculu Q84811 arabidopsis Q95183 arabidopsis Q95183 arabidopsis Q94818 arabidopsis Q94818 arabidopsis Q94818 arabidopsis Q94818 arabidopsis Q94819 Arasagonimus | Q81015 Teeppesvius Q91157 caenorhabdi Q9123 drosophila Q91925 drosophila Q81926 drosophila Q81926 drosophila Q81926 drosophila Q81926 menosoma Q97079 menosoma ci Q9mlh8 paragonimus Q081744 loligo blee Q91841 halocynthia |
|---|---|
| Q8T877 Q8T878 Q9BJ56 Q9BJ56 Q8NVSR3 Q8RWSP63 Q8RWSP63 Q9RBPS Q9RB | Q81013 Q81023 Q81023 Q87387 Q87387 Q87387 Q867 Q867 Q9768 Q9768 Q9768 Q99744 Q99744 |
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ALIGNMENTS

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SEQUENCE FROM N.A.

Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S., Okitani R., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y., Isogai T., Sugano S., "NEDO human cDNA sequencing project.", "NEDO human cDNA sequencing project.", Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=20485419; PubMed=11030752;
Sun M., Goldin E., Stahl S., Falardeau J.L., Kennedy J.C.,
Acierno J.S. Dr., Bove C., Kaneski C.R., Nagle J., Bromley M.C.,
Colman M., Schiffmann R., Slaugenhaupt S.A.;
Wucolipidosis type IV is caused by mutations in a gene encoding a
novel transient receptor potential channel.";
Hum. Mol. Genet. 9:2471-2478 (2000).
                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                         01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein FLJ22449 (Mucolipin) (Mucolipidosis type IV
protein) (Mucolipin 1).
MCOLNI OR MLIV.
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MEDLINE=20428196; PubMed=10973263;
Bargal R., Avidan N., Ben-Asher E., Olender Z., Zeigler M.,
Frumkin A., Ravas-Rothschild A., Glusman G., Lancet D., Bach G.,
"Identification of the gene causing mucolipidosis type IV.";
Nat. Genet. 26:118-121(2000).
                                       580 AA
                                     PRT;
                                     PRELIMINARY;
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                                     09GZU1
RESULT 1
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61 RKPCKLMLQVVKILVVTVQLILFGLSNQLAVTFREENTIAFRHLFLLGYSDGADDTFAAY 120
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                                                          MEDLINE-2048985; PubMed=11013137;
Bassi M.T., Manzoni M., Monti E., Pizzo M.T., Ballabio A., Borsani "Cloning of the game encoding a novel integral membrane protein, mucolipidin, and identification of the two major founder mutations Am. J. Hum. Genet. 67:1110-1120(2000).

EMBL; AJ293970; CAC08215.1;
InterPro; IPR005821; Ion_trans.
InterPro; IPR005821; Ion_trans.
InterPro; IRR005821; Ion_trans.
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           Primates; Catarrhini; Hominidae; Homo
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99.8%; Pred. No. 3.1e-264;
live 0; Mismatches 1;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
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               Strausberg R.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                         Pfam; PF00522; ion trans; 1.
PROSITE; PS00120; IIPASB SER; 1.
Hypothetical protein; Ionic channel; Transmembrane.
SEQUENCE 580 AA; 65022 MW; 7E7691F58D01C804 CRC64;
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tive 0; Mismatches
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                                      EMBL, AK026102, BAB15360.1;
EMBL, AF287269, AAG00797.1;
EMBL, AF287270, AAG00798.1;
EMBL, AF284919, AAG10422.1;
EMBL, BC06149, AAH05149.1;
                                                                                                           Genew; HGNC:13356; MCOLN1.
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Best Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MTAPAGPRGSETERLLTPNPGYGTQAGPSPAPPTPPBEEDLRRLKYFFMSPCDKFRAKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 TREQLYQAIFHAVDQYLALPDVSLGRYAYVRGGGDPWTNGSGLLSASGTTTEATWTR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATLRVALPSVMRFCCCVAVIYLGYCFCGWIVLGPYHVKFRSLSMVSECLFSLINGDDMFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 RKPCKLMLQVVKILVVTVQLILFGLSNQLAVTFREENTIAFRHLFLLGYSDGADDTFAAY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         178 - PITHLTLIRMWLLVNCIQVDPPERPPPPSDDLTLLESSSSYKNLTLKFHKLVNVTIHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RLKTIMLQSLINNEIPDCYTFSVLITFDNKAHSGRIPISLETQAHIQECKHPSVFQHGDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPRLLFDVVVILTCSLSFLLCARSLLRGFLLQNEFVGFMWRQRGRVISLWERLEFVNGWY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ILLVTSDVLTISGTIMKIGIEAKNLASYDVCSILLGTSTLLVWVGVIRYLTFFHNYNILI
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                                                                                                                           MEDLINE=20428196; PubMed=10973263;

MEDLINE=20428196; PubMed=10973263;

MEDLINE=20428196; PubMed=10973263;

A Bargal R., Avidan W., Ben-Asher E., Clender Z., Zeigler M., Frumkin A., Raas-Rothschild A., Glusman G., Lancet D., Bach G.;

T "Identification of the gene causing mucolipidosis type IV.";

T Nat. Genet. 26:118-123 (2000)

E MBL; AF305579; AAG42242.1; JOINED.

R MBL; AF305574; AAG42242.1; JOINED.

R MBL; AF305575; AAG42242.1; JOINED.

R MBL; AF305575; AAG42242.1; JOINED.

R MBL; AF305576; AAG42242.1; JOINED.

R MBL; AF305576; AAG42242.1; JOINED.

R MBL; AF305576; AAG42242.1; JOINED.

R MBL; AF305577; AAG42242.1; JOINED.

R MBL; AF305576; Lacendre Channel TrpL.

R MBL; AF305578; AAG42242.1; JOINED.

R
                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4; Length 581;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00520; ion trans; 1.
PROSITE; PS00120; IIPASE SER; 1.
Ionic channel; Transmembrane.
SEOUENCE 581 AA; 65099 MW; 3.
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Best Local Similarity 94.9
Matches 555, Conservative
  sapiens (Human).
                                                                                      NCBI_TaxID=9606;
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The FANTOM Consortium.

The FANTOM Consortium Research Group Phase I & II Team;

The FANTOM Consortium Research Group Phase I & II Team;

The Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length CDNAs.";

IN Nature 420:563-573(2002).

REMBL; AAGOSS511, AAGOSS511;

REMBL; ARGOSS511, AAGOSS511;

REMBL; ARGOSS511, BACC5922.1;

REMBL; ARGOSS511, BACC5922.1;

REMBL; ARGOSS61, BACC3838.1;

REMBL; ARGOSS61, Mochal.

REMBL; ARGOSS61, Mochal.

RICEPPO; IPRO05211; Can channel TrpL.

RILEPPO; IPRO05211; Can channel TrpL.

RILLEPPO; IPRO05311; Can channel TrpL.

RILLEPPO; IPRO05311; Can channel TrpL.
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MEDLINE=22354683; PubMed=12466851;
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                                                                                                                                          Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .,
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S
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. Falardeau J.L., Kennedy J.C., Acierno J.S., Sun M., Stahl Goldin E., Slaugenhaupt S.A.; "Cloning and characterization of the mouse Mcolni gene.", Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                           TISSUE=Breast tumor;
Strausberg R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00520; ion trans; 1.
PROSITE; PS00120; LIPASE SER; 1.
Ionic channel; Transmembrane.
SEQUENCE 580 AA; 65505 MW; F64D2E6C5D4C041C CRC64;
                               Last sequence update)
Last annotation update)
Created)
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462 YLYSFISLFIYMVLSLFIALITGAYDTIKHPGGAGAEESELQAYIAQCQDSPTSGKFRRG 521
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                246 INNEIPDCYTFSVLITFDNKAHSGRIPISLETQAHIQECK--HPSVFQHGDNSFRLLFDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          272 RHQELPDCYDFTLTITFDNKAHSGRIKISLDNDISIKECKDWHVSGSIQKNTHYMMIFDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67 MLQVVKILVVTVQLILFGLSNQLAVTFREENTIAFRHLFLLGYSDGADDTFAAYTREQLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      187 MVVIDCIQVDPPERPPPPSDDLTLLESSSSYK-NLTLKFHKLVNVTIHFRLKTINLQSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                221 EVBTECFLVEP------DEASHLGTPGENKLNLSLDFHRLLTVELQFKLKAINLQTV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     484 QGRSSLVWLFSQLYLYSFISLFIYMVLSLFIALITGAYDTIKHPGGAGAEESELQAYIAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=C57BL/61; TISSUE=Embryo;
MEDLINE=22354683; PubMed=12466851;
MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of the North CDNAs.";
Nature 420:563-573 (2002)
EMBL; AK035029; BAC29916.1; -.
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53.1%; Score 1628.5; DB 11; Length 594; 55.5%; Pred. No. 1.4e-136; ive 91; Mismatches 121; Indels 39;
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Last sequence update)
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Matches 313; Conservative
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01-MAR-2003 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
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                                                                              SDVLTISGTVWKIGIEAKNLASYDVCSILLGTSTLLWWVGVIRYLFFFKKYNILIATLRV
                                                                                                                                             421 ALPSVMRFCCCVAVIYLGYCFCGWIVLGPYHVKFRSLSMVSECLFSLINGDDMFVTFAAM
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                                              361 SDVLTISGTIMKIGIBAKNLASYDVCSILLGTSTLLVWVGVIRYLTFFHNYNILIATLRV
                                                                                                                                                                                                                                          QAQQGRSSLVWLFSQLYLYSFISLFIYMVLSLFIALITGAYDTIKHPGGAGAEESELQAY
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Bassi M.T., Manzoni M., Monti E., Pizzo M.T., Ballabio A., Borsani ("Cloning of the gene encoding a novel integral membrane protein, mucolipidin, and identification of the two major founder mutations amucolipidin, and identification of the two major founder mutations Am., 1, Hum. Genet. 67:1110-1120(2000).

EMBL: A.293659; CACO78113.1: -.
InterPro; IPR005211; Cat_channel_TrpL.
InterPro; IPR00521; Ion_trans.
Pfam; PP00520; ion_trans.
Ionic channel; Transmembrane.
SEQUENCE 545 AA; 60608 MW; 55179F72029D65C3 CRC64;
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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01-MAR-2001 (TrEMBLrel.
01-OCT-2002 (TrEMBLrel.
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127 QAIFHAVDQYLALPDVSLGRYAYVRGGGDPWTNGSGLALCQRYYHRGHVDPANDTFDIDP 186
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                                                                                                                                  SVMRFCCCVAVIYLGYCFCGWIVLGPYHVKFRSLSMVSECLFSLINGDDMFVTFAAMQAQ
                                        QGRSSLVWLFSQLYLYSFISLFIYMVLSLFIALITGAYDTIKHPGGAGAEESELQAYIAQ
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EMBL: AK033008; BAC28123.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Last sequence update)
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Best Local Similarity 55.59
Matches 313; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Di Palma F., Belyantseva I.A., Kim H.J., Vogt T.F., Kachar B., Noben-Trauth K.;
Noben-Trauth K.;
"Mutaitions in Moclula associated with deafness and pigmentation defects for varitint-waddler (Va) mice.";
Proc. Natl. Acad. Sci. U.S.A. 99:14994-14999(2002).
EMBL; AF475086; AAL84623.1;
EMBL: AY083531; AAM08924.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67 MLQVVKILVVTVQLILFGLSNQLAVTFREENTIAFRHLFLLGYSDGADDTFAAYTREQLY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39; Gaps
                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Falardeau J.L., Kennedy J.C., Acierno J.S., Slaugenhaupt "Cloning of the mouse Mcoln3 gene.", Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  553 AA; 63748 MW; 8E257B05D96DF536 CRC64;
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InterPro; IPR002111; Cat channel TrpL.
InterPro; IPR005821; Ion_trans.
Pfam; PF00520; ion_trans, 1.
Ionic channel; Transmembrane.
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STRAIN=C57BL/6J;
MEDLINE=22317414; PubMed=12403827;
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Mammalia; Eutheria; Rodentia;
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01-JUN-2002 (TrEMBLrel. 21,
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                                                                                                                                          PRELIMINARY;
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                                                    545 QDSPTSGKFRRGSGSACSLLCCC 567
                                                                                                     569 KDLPNSGKYRLEDDPPGSLLCCC 591
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01-JUN-2002 (TrEMBLrel. 21,
01-OCT-2002 (TrEMBLrel. 22,
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                                                      67 MLQVVKILVVTVQLILFGLSNQLAVTFREENTIAFRHLFLLGYSDGADDTFAAYTREQLY 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  272 HOELPDCYDFTLTITFDNKAHSGRIKISLDNDISIKECKDWHVSGSIQKNTHYMMIFDAF 331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            425 VMRFCCCVAVIYLGYCFCGWIVLGPYHVKFRSLSMVSBCLFSLINGDDMFVTFAAMQAQQ 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  484 QGRSSLVWLFSQLYLYSFISLFIYMVLSLFIALITGAYDTIKHPGGAGAEESELQAYIAQ 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  220 EVETECFLVBPDE------DSHLGTPGENKLNLSLDFHRLLTVELQFKLKAINLQTVR 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The FANTOM Consortium, the RIKEN Genome Exploration Research Group Phase I & II Team; the RIKEN Genome Exploration Research Group Phase I & II Team; Whallysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573 (2002).

EMBL: AK030819; BAC27146.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52.9%; Score 1623.5; DB 11; Length 593;
55.4%; Pred. No. 3.9e-136;
iive 89; Mismatches 125; Indels 37; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               593 AA; 68255 MW; F3708D6B5429E9BF CRC64;
                                                                                                                                                                                                                                                                                                                                                            01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                593 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                         Weakly similar to MUCOLIPIDIN (Fragment).
                                                                                                                                                                                  566 CKDLPNSGKYRLEDDPPGSLLCCC 589
                                                                                                                                544 CODSPISGKFRRGSGSACSLLCCC 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-Thymus;
MEDLINE-22354683; PubMed-12466851;
                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      al Similarity 55.4° 312; Conservative
                                                                                                                                                                                                                                                                                                                PRELIMINARY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QNEFVGFWWRQRGRVISLWERLEFVNGWYILLVTSDVLTISGTIMKIGIEAKNLASYDVC 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          149 YVRGGGDPWTNGSGLALCQRYYHRGHVDPANDTFDIDPMVVTDCIQVDPPERPPPPSDD 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              254 GRIKISLDNDISIRECKDWHVSGSIQKWTHYMMIFDAFVILTCLVSLILCIRSVIRGLQL 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    314 QQEFVNFFLLHYKKEVSVSDQMEFVNGWYIMIIISDILTIIGSILKMEIQAKSLTSYDVC 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          387 SILLGTSTLLVWVGVIRYLTFFHNYNILIATLRVALPSVMRFCCCVAVIYLGYCFCGWIV 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      447 LGPYHVKFRSLSMVSECLFSLINGDDMFVTFAAMQAQQGRSSLVWLFSQLYLYSFISLFI 506
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26 TSPSEELLLEDOMRRKLKFFFMNPCEKFWARGRKPWKLAIQILKIAMVTIQLVLFGLSNQ 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34 TPPEEE----DLRRRLKYFFMSPCDKFRAKGRKPCKLMLQVVKILVVTVQLILFGLSNQ 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             146 YENKG----TKOSAMAICOHFYKRGNIYPGNDTFDIDPEIETECFFVEPDE----PFHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                197 GTPAENK---LNLTLDFHRLLTVELQFKLKAINLQTVRHQELPDCYDFTLTITFDNKAHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       209 LTLLESSSSYKNLTLKFHKLVNVTIHFRLKTINLOSLINNEIPDCYTFSVLITFDNKAHS
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                                                                                                                                                          Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22;
                                                                                                                                                                                                                                                                                                                                                                     Falardeau J.L., Kennedy J.C., Acierno J.S., Slaugenhaupt S.A., "Cloning of the MCOLN3 gene.";
"Cloning of the MCOLN3 gene.";
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AF475085, AAB4652.1;
InterPro; IPR002111; Cat channel TrpL.
InterPro; IPR005821; Ion trans.
Ffam, PF00520, ion trans.
Ionic channel, Transmembrane.
SEQUENCE S53 AA; 64247 MW; 2E63DA196379F9B3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 553;
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Last sequence update)
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PRT;
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567 C 567
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 209 LTLLESSSSYKNLTLKFHKLVNVTIHFRLKTINLQSLINNEIPDCYTFSVLITFDNKAHS 268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                435 YMILSLFIALITDTYETIKQYQQDGFPETELRTFISECKDLPNSGKYRLEDDPPVSLFCC 494
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34 TPPEEE-----DLRRRLKYFFMSPCDKFRAKGRKPCKLMLQVVKILVVTVQLILFGLSNQ 88
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R MBL; AKO01868; BAA919511; -- Ishii. -- InterPro; IPRO02111; Cat_channel_TrpL.

R InterPro; IPRO02111; Cat_channel_TrpL.

R Pfam; PF00520; ion trans.

R SEQUENCE 497 AA; 57739 MW; 3128395B50E5890D CRC64;
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                                                                                                                                                                                                                                                                           Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37 EEEDLRRRLKYFFMSPCDKFRAKGRKPCKLMLQVVKILVVTVQLILFGLSNQLAVTFREE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 KEBCLKEDLKFYFMSPCEKYRARRQIPWKLGLQILKIVMVTTQLVRFGLSNQLVVAFKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97 NTIAFRHLFLLGYSDGADDTF - AAYTREQLYQAIFHAVDQYLALPDVSLGRYAYVRGGG
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE-22317414; PubMed=12403827;
Di Pella F., Belyantseva I.A., Kim H.J., Vogr T.F., Kachar
Noben-Trauth K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in varitint-waddler (Va) mice.";
Proc. Natl. Acad. Sci. U.S.A. 99:14994-14999 (2002).
EMBL; AY08353; AAM08926.1; - SEQUENCE 538 AA; 62684 MW; 1BCCB92F8D6C83C4 CRC64;
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Mucolipin 2.
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276 ETQAHIQECKHPSVFQHGDNS--FRLLFDVVVILTCSLSFLLCARSLLRGFLLQNEFVGF 333
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330002C04RIK OR MCOLN2.
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EMBL; AKO14954; BAB31730.1;
EMBL; AKO14967; BAB2972.1;
EMBL; AKO14967; BAB2972.1;
EMBL; AKO14967; BAB29372.1;
Interpro; IPRO0111; Cat_channel_TrpL.
Interpro; IPRO0521; Ion_trans.
Interpro; IPRO0520; ion_trans.
Ionic channel; Transmembrane.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                    01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 23, Last annotation update)
030000200481k protein (Mucolipin 2).
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                                      PRELIMINARY;
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                                                                                                   238 NSEANIEECKNAMISGSTQRSTHYLLVFDVFVIMICLASLILCTRSIVLALRLRKRFLNF 297
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216 SSYKNLTLKFHKLVNVTIHFRLKTINLQSLINNEIPDCYTFSVLITFDNKAHSGRIPISL 275
                                                                                                                                                                                                                                                                                                                   276 ETQAHIQECKHPSVFQHGDNS--FRLLFDVVVILTCSLSFLLCARŞLLRGFLLQNEFVGF 333
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EMBL, AFS03575, AAM28596.1, -.
MGD, MGI:1915529, 3300000004Rik.
InterPro, IPR002111; Cat channel TrpL.
SEQUENCE 566 AA; 65449 MW; 314CEC662B3BDC07 CRC64;
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Last annotation update)
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                                                                                       FLEKYKQRVCGADQM---EFVNGWYVLVTISDLMTIIGSILKWEIKAKKLTNYDVCSILL 382
                                                                                                                                                                                                                                                          443 HEKFENLNIVAECLFSLVNGDDMFATFA--QIQQ-KSILVWLFSRLYLYSFISLFIYWVL 499
                                                                                                                                                                                                                                                                                                                                  SLFIALITDSYHTIKKYQQHGFPETDLQKFL---KESGSKDGYQKQPSALLSCLCCLRRR 556
266 NSEANIEECKNWNISGSTQRSTHYLLVPDVFVIMICLASLILCTRSIVLALRRRREINF 325
                                                                  334 M---WRORGRVISLWERLEFVNGWYILLVTSDVLTISGTIMKIGIEAKNLASYDVCSILL 390
                                                                                                                                                 GTSTLLVWVGVIRYLTFFHNYNILIATLRVALPSVMRFCCCVAVIYLGYCFCGWIVLGPY 450
                                                                                                                                                                                     383 GISTLEVWVGVIRYLGYFQTYNVLILTMQASLPKVLRFCACAGMIYLGYTFCGWIVLGPY 442
                                                                                                                                                                                                                              HVXFRSLSMVSECLFSLINGDDMFVTFAAMQAQQGRSSLVWLFSQLYLYSFISLFIYMVL 510
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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43.4%; Score 1332; DB 11; Length 538;
Best Local Similarity 49.1%; Pred. No. 3.5e-110;
Matches 270; Conservative 102; Mismatches 150; Indels 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.;
Strausberg R.;
Strausberg R.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC029847; AAH29847.1;
GMS.; BC029847; AAH29847.1;
GMS.; MGI:1915529; 3300002C04Rik.
InterPro: IPR002111; Cat channel TrpL.
SEQUENCE 538 AA; 62296 MW; 861C081FE96A628B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
RIKEN cDNA 3300002C04 gene.
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557 RSNDHLILID 566
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SEQUENCE FROM N.A.
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                                                                                                                                                                511 SLFIALITGAYDTIKHPGGAGAEESELQAYIAQCQDSPTSGKFRRGSGSACSLLCCCGRD 570
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                                                                                  HVKFRSLSMVSECLFSLINGDDMFVTFAAMQAQQGRSSLVWLFSQLYLYSFISLFIYMVL
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529 RNNDHLILID 538
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
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| orgonom memin |)))) | (I) | phila r | 'O | TANGO | adv [od | SPCTPTPD | human | human | human - | | liver | brain expr | 85 enc | immune/haem | human diagn | phila | Mouse Polycystin-2 | 200 | e polycystic | liver pent | #101 | 9662# u | rain ex | pone | Peptide #10504 enc | peptide e | acrosom | | Peptide #5191 enco | polycyst | acrosome re | acid sequ | Polycy | liver p | Peptide #8717 enco |
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| 10 | :- | 4 6 | 77 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | | . 41 | 42 | 43 | 44 | 45 |

ALIGNMENTS

antiinflammatory; anticonvalsant; immunosuppressive; antidiarrheic; antiarteriosclerotic; gene therapy; cell proliferative disorder; autoimmune disorder; inflammatory disorder; neurological disorder; epilepsy; diarrhoea. membrane associated protein; MEMAP; diagnosis; cytostatic; Burford N, Azimzai Y; Human membrane associated protein MEMAP-13. Yue H, Tang YT, Bandman O, IR, Lu DAM, Patterson C; AAB74707 standard; Protein; 580 AA. 99US-0149641. 99US-0164203. (INCY-) INCYTE GENOMICS INC. 14-AUG-2000; 2000WO-US22315. 12-JUN-2001 (first entry) WO200112662-A2 Homo sapiens. 17-AUG-1999; 09-NOV-1999; 22-FEB-2001. Lal P, Yue Baughn MR, AAB74707;

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481 QAQQGRSSLVWLFSQLYLYSFISLFIYWVLSLFIALITGAYDTIKHPGGAGAEESELQAY 540
                                                  IAQCQDSPTSGKFRRGSGSACSLLCCCGRDPSEEHSLLVN
                                                                                                                                                                                                                                                 Human TLCC-2 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                              calcium signaling.
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                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
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                                                                                                                                                                       containt to AAPT41/1/ encode the human membrane associated proteins (MEMAP) given in AAB74655 to AAB74731. MEWAPS have cytostatic.

antianteriosclerotic activities, which can be used in gene therapy.

Contining and agonist of MEMAPS can be used to reat a disease or condition associated with decreased expression of functional MEMAP and antagonists of MEMAPs are used to treat a disease or condition associated with decreased expression of functional MEMAP and antagonists of MEMAP are used to treat a disease or condition associated with overexpression of functional MEMAP. These disorders include cell proliferative, autoimmune/inflammatory, neurological and gastrointestinal proliferative, autoimmune/inflammatory, neurological and gastrointestinal proliferative, autoimmune/inflammatory, neurological and gastrointestinal disorders. Specific examples of these disorders included cancer, inflammaton, atheroselerosis, epilepsy and diarrhoea. MEMAP proteins can be used to screen for compounds which specifically building antibodies, oligomicleotides, otherwise and small molecules. MEMAP polymucleotides can be used to prepare transgenic disease. Anti-MEMAP protein and can be used to prepare transgenic detection of MEMAP protein and can be used as antagonists to treat or prevent a disorder associated with MEMAP. Polymucleotides encoding MEMAP. Can be expression of MEMAP to treat or prevent a disorder associated with genetic abnormalities with respect with MEMAP.
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                                                           Isolated polypeptide with a human membrane associated protein sequence is useful for the diagnosis, prevention and treatment of cell proliferative, autoimmune/inflammatory, neurological and
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Pred. No. 0;
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                                                                                                                                       Claim 1; Page 125-126; 173pp; English
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                                                                                                           gastrointestinal disorders
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               WPI; 2001-168860/17.
N-PSDB; AAF81753.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a novel transient receptor potential (TRP)-like calcium Channel, designated TLGC-2 and polynucleorides encoding the TLGC-2. TLGC-2 can be expressed by standard recombinant methodology. The TLGC-2 polypeptide, polynucleotides and medulators are useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transient receptor potential like calcium channel; TRP; TLCC-2; human; neuroprotective; analgesic; nootropic; antiparkinsonian; antidepressant; cerebroprotective; anxiolytic; antimanic; anticonvulsant; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MTAPAGPRGSETERLLIPNPGYGTQAGPSPAPPTPPEEEDLRRRLKYFFMSPCDKFRAKG
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541 IAQCQDSPISGKFRRGSGSACSLLCCCGRDPSEEHSLLVN
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                                                                                                                                                                                                     ABB07816 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-338931/37.
N-PSDB; ABL40754, ABL40755.
                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CURT/) CURTIS R A J. (SILO/) SILOS-SANTIAGO I.
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            TREQLYQAIFHAVDQYLALPDVSLGRYAYVRGGGDPWTNGSGLALCQRYYHRGHVDPAND
                                                   FDVVVILTCSLSFLLCARSLLRGFLLQNBFVGFMWRQRGRVISLWBRLBFVNGWYILLVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                      nociception, nootropic, neuroprotective; antiparkinsonian; cytostatic, hypotensive, antidepressant; analgesic; anticonvulsant; tranquiliser; Parkinson's disease; Huntington's disease; multiple sclerosis; Gilles de la Tourette's syndrome; autonomic function disorder; neuroleptic; gene therapy; Alzheimer's disease; CNS disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel isolated human transient receptor potential-like calcium channel protein-2 useful for treating Alzheimer's disease, depression, amnesia,
                                                                          TPDIDPMVVIDCIQVDPPERPPPPSDDLTLLESSSSYKNLTLKFHKLVNVTIHFRLKTI
                                                                                                               NLQSLINNEIPDCYTFSVLITFDNKAHSGRIPISLETQAHIQECKHPSVFQHGDNSFRLL
                                                                                                                                                                 PDVVVILTCSLSFLCARSLLRGFLLQNBFVGFWWRQRGRVISLWERLEFVNGWYILLVT
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                                                                                                                                                                                                       361 SDVLTISGTIMKIGIBAKNLASYDVCSILLGTSTLLVWVGVIRYLTFFHNYNILLATLRV
                                                                                                                                                                                                                           ALPSVMRFCCCVAVIYLGYCFCGWIVLGPYHVKFRSLSMVSECLFSLINGDDMFVTFAAM
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                                                                                                                                                                                                                                                                                                                                                                                                                            Human TRP-like calcium channel TLCC-2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MILL-) MILLENIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-010913/01.
N-PSDB; AAI71699, AAI71700.
                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                              TLCC-2;
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                                             The present invention relates to the protein and coding sequences of human transient receptor potential (TRP)-like calcium channel protein-2 (TLC-2). The sequences can be used in the treatment of TLC-2 related disorders, including central nervous system disorders such as Alzheimer's, Parkinson's and Huntington's diseases, multiple sclerosis, Gilles de la Tourette's syndrome, autonomic function disorders, learning or memory disorders, pain disorders and disorders of cellular proliferation, including cancer. The present sequence is the TLCC-2
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7; Fig 1; 148pp; English.
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cardiant; gene therapy, cancer, immune disorder; cardiovascular disorder, neurological disease; infection; human; secreted protein.
                                                                                                                                                                                                            Novel 1405 isolated polypeptides, useful for diagnosis, treatment and
                                                                                                                                                                                                                       prevention of neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferative
vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic;
                                                                                                                                                                                                                                                              Claim 11; SEQ ID NO 2325; 2081pp + Sequence Listing; English
                                                                                                                                          (HUMA-) HUMAN GENOME SCI INC.
                                                                                                  18-MAY-2001; 2001WO-US16450.
                                                                                                                      19-MAY-2000; 2000US-205515P.
                                                                                                                                                             Rosen CA;
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                                                                                                                                                                                            N-PSDB; ABL90358
                                                           WO200190304-A2
                                         Homo sapiens.
                                                                              29-NOV-2001
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The invention relates to novel genes (ABL89449-ABL90853) and proteins (ABB89040-ABB90444) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune chamber thyroiditis, diabetes mellitus, Crohn's disease, miltiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial isohaemias; ed, wound healing; (e) neurological diseases e.g. cerebral anoxia and epidensy; and (f) infectious diseases such as viral, bacterial, fungal Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences. and parasitic infections.

511 AA; Sequence

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                                                                                   70 VVKILVVTVQLILFGLSNQLAVTFREENTIAFRHLFLLGYSDGADDTFAAYTREQLYQAI
                                                                                                                    1 MVKILVVTVQLILFGLSNQLAVTFREENTIAFRHLFLLGYSDGADDTFAAYTREQLYQAI
                                                                                                                                                           FHAVDQYLALPDVSLGRYAYVRGGGDPWTNGSGLALCQRYYHRGHVDPANDTFDIDPMVV
                                                                                                                                                                                 61 FHAVDQYLALPDVSLGRYAYVRGGGDPWTNGSGLALCQRYYHRGHVDPANDTFDIDPMVV
                                                                                                                                                                                                                                      TDCIQVDPPERPPPPSDDLTLLESSSSYKNLTLKFHKLVNVTIHFRLKTINLQSLINNE
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                                                0; Gaps
             Score 2685; DB 23; Length 511; Pred. No. 3.2e-281;
                                                Indels
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87.5%; Scor.
99.8%; Pred. No. 3.c.
                                                Matches 510; Conservative
               Query Match
Best Local Similarity
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The polynucleotide sequences given in AAA39052 to AAA39088 encode the human secreted proteins given in AAB08891 to AAB08984. The human secreted proteins can have activities based on the tissues and cells they are expressed in. Examples of the activities are: cytostatic, and they are anti-proliferative; immunosuppressive, antibacterial, and vulnerary. The secreted proteins and their related polynucleotide sequences are useful for diagnostic and therapeutic methods useful for diagnostic and therapeutic methods useful for diagnostic and treating
                                301 IMKIGIBAKNLASYDVCSILLGTSTLLVWVGVIRYLTFFHNYNILIATLRVALPSVMRFC 360
                                                                               489
                                                                                                                    361 CCVAVIYLGYCFCGWIVLGPYHVKFRSLSMVSECLFSLINGDDMFVTFAAMQAQQGRSSL 420
                                                                                                                                                             VWLFSQLYLYSFISLFIYMVLSLFIALITGAYDTIKHPGGAGAEESELQAYIAQCQDSPT 549
                                                                                                                                                                                                   421 VWLFSQLYLYSFISLFIYMVLSLFIALITGAYDTIKHPGGAGAEESELQAYIAQCQDSPT 480
370 IMKIGIEAKNLASYDVCSILLGTSTLLVWVGVIRYLTFFHNYNILIATLRVALPSVMRFC 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    bind to the proteins. The proteins or polynucleotide sequences may be used as food additives or preservatives, to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, co-factors or other nutritional components. Agonists or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disorders related to the secreted proteins. The proteins, and polymorleotide sequences may be useful for treating disorders of the immune system, hyperproliferative disorders, infectious disease, regeneration of tissues, for chemotaxis and for screening molecules that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; secreted protein; cytostatic; anti-proliferative; vulnerary; immunosuppressive; antibacterial; diagnosis; immune system; chemotaxis; hyperproliferative disorder; infectious disease; tissue regeneration; screening; food additive; preservative; wound healing; hyper-vascular disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human secreted proteins and coding sequences useful in diagnostic and therapeutic methods for disorders such as immune system or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ni d;
                                                                               CCVAVIYLGYCFCGWIVLGPYHVKFRSLSMVSECLFSLINGDDMFVTFAAMQAQQGRSSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human secreted protein sequence encoded by gene 16 SEQ ID NO:63.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         proliferative disorders, related to the proteins
                                                                                                                                                                                                                                                 SGKFRRGSGSACSLLCCCGRDPSEEHSLLVN 580
                                                                                                                                                                                                                                                                      481 SGKFRRGSGSACSLLCCCGRDPSEEHSLLVN 511
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Soppet DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 11; Page 362-363; 416pp; English.
                                                                                                                                                                                                                                                                                                                                                                                        AAB08906 standard; Protein; 511 AA.
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98US-0102895.
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antagonists of the proteins may be used to prevent scar tissue growth during wound healing, and hyper-vascular diseases. AAA39043 to AAA39051 and AAB088890 are sequences used in the exemplification of the present
                                                                                                                                                                                                                               FHAVDQYLALPDVSLGRYAYVRGGGDPWTNGSGLALCQRYYHRGHVDPANDTFDIDPMVV
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                                                                                                                                                                    TOCIQUOPPERPPPPSDDLTLLESSSSYKNLTLKFHKLVNVTIHFRLKTINLQSLINNE
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                                                                                                                                                                                                                                                                                                                                                                                          SLSFLLCARSLLRGFLLQNEFVGFWWRQRGRVISLWERLEFVNGWYILLVTSDVLTISGT
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                                                                                                                                                                                                       FHAVDQYLALPDVSLGRYAYVRGGGDPWTNGSGLALCQRYYHRGHVDPANDTFDIDPMVV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  IMKIGIEAKNLASYDVCSILLGTSTLLVWVGVIRYLTFFHNYNILIATLRVALPSVMRFC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCAAVIYLGYCFCGWIVLGPYHVKFRSLSMVSECLFSLINGDDMFVTFAAMQAQQGRSSL
                                                                                                                               Gaps
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                                                                                                Score 2661; DB 21; Length 511;
Pred. No. 1.3e-278;
1; Mismatches 4; Indels 0
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                                                                                                 86.8%;
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                                                                                                                        Matches 506;
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99JP-0248036. 99JP-0300253. 2000JP-0118776. 2000JP-0183767.

27-AUG-1999; 11-JAN-2000;

2000JP-0241899

02-MAY-2000; 09-JUN-2000;

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The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dr primer and an oligonucleotide comprises one of the complementary strand of a polynucleotide which comprises one of oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5-end of sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'end sequence. Where the oligonucleotide comprises a 1'end sequence, where the combination of the 5'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs. The primers allow obtaining the cDNAs assily whences, and any appectation and cDNAs administration of the full-le
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB95893 represent human amino acid sequences, and AAH13629 to AAH13632 represent oligonuclectides, all of which are used in the exemplification
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                                                                                                                                                                                          Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89 LAVTFREENTIAFRHLFLLGYSDGADDTFAAYTREQLYQAIFHAVDQYLALPDVSLGRYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   149 YVRGGGDPWTNGSGLALCQRYYHRGHVDPANDTFDIDPMVVTDCIQVDPPERPPPPSDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26 TSPSEBLLIBDQMRRKLKPFPMNPCEKFWARGRKFWKLAIQILKIAMVII------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34 TPPESE-----DLRRRLKYFFMSPCDKFRAKGRKPCKLMLQVVKILVVTVQLILFGLSNQ
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                                                                             Yamamoto
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                                                                           Saito K,
Otsuki
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51.2%; Pred. No. 1.2e-141;
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                                                                                                                                                                                                                                                                                                                Claim 8; SEQ ID 12616; 2537pp + CD ROM; English.
                                                                           Hayashi K, S
A, Nagai K,
                                                                        hikawa T, Hay
Wakamatsu A,
                                                                      Nishikawa '
T, Wakama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the present invention.
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                                                                        Isogai T,
Sugiyama
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Ishii S,
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                                                                                                                                                                                           human; antidiabetic; antiarteriosclerotic; anorectic; nootropic;
  LGPYHDKFRSLNMVSECLFSLINGDDMFATFAKWQQ---KSYLVWLFSRIYLYSFISLFI
                          YMVLSLFIALITGAYDTIKHPGGAGAEESELQAYIAQCQDSPTSGKFRRGSGSACSLLCC
                                     Shenoy SG, Kekuda R, Rastelli L, Mezes PD, Smithson ach V, Casman SJ, Boldog EL, Li L, Zerhusen BD; Gangolli EA, Vernet CAM, Spytek KA, Malyankar UM; Miller CE, Taupier RJ, Heyes MP, Ju J, Peyman JA; MacDougall JR, Edinger SR, Stone DJ, Mazur A;
Human NOV9c CG90709-03 protein SEQ ID
                                                                                                                                                                                                                                               netabolic syndrome X; wasting disease.
                                                                                                                        ABU12053 standard; Protein; 538 AA
                                                                                                                                                                                                                                                                                                                                            2001US - 281906P
2001US - 282020P
2001US - 283444P
2001US - 283512P
2001US - 28531P
2001US - 28531P
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2002US-345755P.
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This invention describes novel polypeptides, termed NOVX which have antidiabetic, antiarteriosclerotic, anorectic, metabolic, antimicrobial, entidiabetic, antiparkinsonian, antilipaemic, cytostatic, nootropic, cardiant and immunomodulatory activity. The polypeptide and any cardiant and immunomodulatory activity. The polypeptide and any contibodies generated from it are useful in the manufacture of a medicament for treating a syndrome associated with a human disease.

Selected from a pathology associated with the NOVX polypeptide. Fragments and portions of the polymucleotides encoding NOVX polypeptides. Fragments and portions of the polymucleotides encoding NOVX polypeptides are useful to the map the location of NOVX genes on a chromosome, to identify crestriction fragment length polymorphism (RFLP), and are useful to restriction fragment length polymorphism (RFLP), and are useful to prepare polymerase chain reaction primers. The products of the invention can be used in gene therapy and for treating cardiomyopathy, metabolic disorders, disease, anorexia, neurodegenerative disorders, Alebaners, and various disease, anorexia, neurodegenerative disorders, Alebaners, and various cancexia, metabolic distributabances associated with obesity, metabolic syndrome X and wasting disorders associated with chronic diseases and various cancers. ABU12041-ABU12086 represent the polypeptide fragments concoded by the NOVX polynucleotides represented in ABX55261-ABX55306.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69 NTVAFKHLFLKGYSGTDEDDYSCSVYTQEDAYESIFFAINQYHQLKDITLGTLGY---G 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      155 DPWTNGSGLALCQRYYHRGHVDPANDTFDIDPMWVTDCIQVDPPERPPPPSDDLTLLES
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                                                                                                                                                                Claim 1; Page 112; 425pp; English.
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EEHSLLVN 580

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Human NOV9d CG90709-04 protein SEQ ID 28
                                                                                                                                                                     ABU12054 standard; Protein; 566
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                             538
19-FEB-2003
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ABU12054
ID ABU12054
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XXX NOVY
KW MECK
KW CARK
KW CAR
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NOVX; human; antidiabetic; antiarteriosclerotic; anorectic; nootropic; metabolic; antimicrobial; neuroprotective; antiparkinsonian; cardiant; antilipaemic; cytostatic; immunomodulacory; gene therapy; dyslipidaemia; cardiomyopathy; metabolic disorder; diabetes; atherosclerosis; obesity; anorexia; neurodegenerative disorder; Alzheimer's disease; cancer; Parkinson's disease; haematopoietic disorder; metabolic disturbance; metabolic syndrome X; wasting disease

Homo sapiens

WO200281625-A2

17-OCT-2002

03-APR-2002; 2002WO-US10366 03-APR-2001;

2001US -281906P 2001US -882020P 2001US -283444P 2001US -283444P 2001US -283612P 2001US -28367P 2001US -28367P 2001US -28367P 2001US -28381P 2001US -28532SP 2001US -286292P 13-APR-2001; 10-APR-2001; 3-APR-2001; 13-APR-2001; 9-APR-2001; 30-APR-2001; 35-APR-2001; 05-APR-2001 06-APR-2001 .7-APR-2001

2001US-311973P. 2001US-312901P 001US-322283P 001US-345734P 2001US-327448P 26-JUN-2001; 13-AUG-2001; 16-AUG-2001; 4-SEP-2001; 05-OCT-2001

37-JUN-2001;

(CURA-) CURAGEN CORP.

u M, Shenoy SG, Kekuda R, Rastelli L, Mezes PD, Smithson Gerlach V, Casman SJ, Boldog FL, Li L, Zerhusen BD; v VT, Gangolli EA, Vernet CAM, Spytek KA, Malyankar UM; Jan M, Miller CE, Taupier RJ, Heyes MP, Ju J, Peyman JA; on E, MacDougall JR, Edinger SR, Stone DJ, Mazur A; Tchernev VT, C Patturajan M, Catterton E, Padigaru M,

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WPI; 2003-046862/04. N-PSDB; ABX56274 New isolated NOVX polypeptide useful for treating cardiomyopathy, atherosclerosis, metabolic disorders, diabetes, obssity, infectious disease, anorexia, neurodegenerative disorders, Alzheimer's disease and

Claim 1; Page 113; 425pp; English

antidiabetic, antiarteriosclerofic, anorectic, metabolic, antimicrobial, neuroprotective, antiparkinsonian, antilipaemic, cytostatic, nootropic, cardiant and immunomodulatory activity. The polypeptide and any antibodies generated from it are useful in the manufacture of a medicament for treating a syndrome associated with a human disease selected from a pathology associated with the NoVX polypeptide. Fragments and portions of the polymclectides encoding NOVX polypeptides are useful to map the location of NOVX genes on a chromosome, to identify restriction fragment length polymorphism (RFLP), and are useful to prepare polymerase chain reaction primers. The products of the invention can be used in gene therapy and for treating cardiomyopathy, metabolic disorders, diabetes, albarosclerosis, obsesty, infectious disease, anorexa, immuno disorders, Alzheimer's disease, anorexa, immuno disorders, Alzheimer's disease, parkinson's ώ ώ 97 NTIAFRHLFLLGYSDGADDTF--AAYTREQLYQALFHAVDQYLALPDVSLGRYAYVRGGG 154 152 275 LETQAHIQECKHPSVFQHGDNS--FRLLFDVVVILTCSLSFLLCARSLLRGFLLQNEFVG 332 metabolic 208 SSFFR---LEFYRLLQVBISFHLKGIDLQTIHSRELPDCYVFQNTIIFDNKAHSGKIKIY 264 452 384 572 96 96 558 disease, immune disorders, haematopoietic disorders, and various dyslipidaemias, metabolic disturbances associated with obesity, metabol syndrome X and wasting disorders associated with chronic diseases and various cancers. ABU12041-ABU12086 represent the polypeptide fragments encoded by the NOVX polynucleotides represented in ABX56261-ABX56306. 37 BEEDLRRRLKYFFMSPCDKFRAKGRKPCKLMLQVVKILVVTVQLILFGLSNQLAVTFREE 155 DPWINGSGLALCQRYYHRGHVDPANDIFDIDPMVVTDCIQVDPPERPPPPSDDLTLLES 215 SSSYKNLTLKFHKLVNVTIHFRLKTINLQSLINNEIPDCYTFSVLITFDNKAHSGRIPIS 325 FFLEKYKRPVCDTDQWEFINGWYVLVIISDLMTIIGSILKMEIKAKNLTNYDLCSIFLGT PMWRQRGRVISLWERLEFVNGWYILLVTSDVLTISGTIMKIGIEAKNLASYDVCSILLGT STILLVWVGVIRYLTFFHNYNILLATLRVALPSVMRFCCCVAVIYLGYCFCGWIVLGPYHV Gaps KFRSLSMVSECLFSLINGDDMFVTFAAMQAQGRSSLVWLFSQLYLYSFISLFIYMVLSL 445 KFENLNTVAECLFSLVNGDDMFATFA--QIQQ-KSILVWLFSRLYLYSFISLFIYMILSL PIALITGAYDTIKHPGGAGAEESELQAYIAQCQDSPTSGKFRRGSGSACSLLCCCGRDPS invention describes novel polypeptides, termed NOVX which have 22; Length 566; Indels Query Match
44.6%; Score 1368; DB 24;
Best Local Similarity 48.7%; Pred. No. 1.6e-138;
Matches 267; Conservative 115; Mismatches 144; EEHSLLVN 580 566 AA; 333 Sequence 393 385 573 453 513 502 8 ద d ö g g ò ò $\overset{\circ}{\circ}$ $\overset{\circ}{\circ}$ g g ઠે $\overset{\circ}{\circ}$ 임 ò Db ò

ABU12052 standard; Protein; 544 AA. RESULT 9
ABU12052
ID ABU11

SIdI'HQQ

ABU12052;

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Human NOV9b CG90709-02 protein SEQ ID 24.
 19-FEB-2003 (first entry)
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metabolic; antimicrobial; neuroprotective; antiparkinsonian; cardiant; antilipaemic; cytostatic; immunomodulatory; gene therapy; dyslipidaemia; cardiomyopathy; metabolic disorder; diabetes; atherosclerosis; obesity; anorexia; neurodegenerative disorder; Alzheimer's disease; cancer; Parkinson's disease; haematopoietic disorder; metabolic disturbance; metabolic syndrome X; wasting disease. NOVX; human; antidiabetic; antiarteriosclerotic; anorectic; nootropic; 03-APR-2002; 2002WO-US10366 WO200281625-A2. 13-APR-2001; .3-APR-2001; Homo sapiens 13-APR-2001; 17-OCT-2002

10-APR-2001; 2001US-282930P. 12-APR-2001; 2001US-28344P. 12-APR-2001; 2001US-283512P. 2001US-283657P. 2001US-284234P. 2001US-286068P 2001US-286292P 2001US-300883P 2001US-311003P. 2001US-312901P 2001US-322283P. 2001US-327448P 2001US-345734P. 2002US-345755P 2002US-354391P 05-APR-2001; 2001US-281906P 06-APR-2001; 2001US-282020P 2001US-283678P 2001US-283710P 2001US-285325P 2001US-285381P 26-JUN-2001; 16-AUG-2001; 17-APR-2001; 24-APR-2001; 14-SEP-200

(CURA-) CURAGEN CORP.

Padigaru M, Shenoy SG, Kekuda R, Rastelli L, Mezes PD, Smithson G; Guo X, Gerlach V, Casman SJ, Boldog FL, Li L, Zerhusen BD; Tchernev VT, Gangolli EA, Vernet CAM, Spytek KA, Malyankar UM; Patturajan M, Miller CE, Taupier RJ, Heyes MP, Ju J, Peyman JA; Catterton E, MacDougall JR, Bdinger SR, Stone DJ, Mazur A;

WPI; 2003-046862/04. N-PSDB; ABX56272 New isolated NOVX polypeptide useful for treating cardiomyopathy, atherosclerosis, metabolic disorders, diabetes, obesity, infectious disease, anorexia, neurodegenerative disorders, Alzheimer's disease and

Claim 1; Page 111; 425pp; English.

antidiabetic, antiarteriosclerotic, anorectic, metabolic, antimicrobial, neuroprotective, antiparkinsonian, antilipaemic, cytostatic, nootropic, cardiant and immunomodulatory activity. The polypeptide and any antibodies generated from it are useful in the manufacture of a medicament for treating a syndrome associated with a human disease selected from a pathology associated with the NoVX polypeptide. Fragments This invention describes novel polypeptides, termed NOVX which have

NOVX; human; antidiabetic; antiarteriosclerotic; anorectic; nootropic; metabolic; antimicrobial; neuroprotective; antiparkinsonian; cardiant;

Human NOV9a CG90709-01 protein SEQ ID 22

(first entry)

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ABU12051 standard; Protein; 540

ABU1205

to map the location of NOVX genes on a chromosome, to identify the individuals from minute biological samples, as DNA markers for restriction fragment length polymorphism (RTLP), and are useful to prepare polymerase chain reaction primers. The products of the invention can be used in gene therapy and for treating cardiomyopathy, metabolic disorders, diabeters, atherosclerosis, obesity, infectious disease, anorexia, neurodegenerative disorders, hlzbeimer's disease, Parkinson's disease, immune disorders, haematopoietic disorders, and various dyslipidaemias, metabolic disturbances associated with obesity, metabolic syndrome X and wasting disorders associated with chronic diseases and various cancers. Abula-Abul2000 represent the polypeptide fragments encoded by the NOVX polynucleotides represented in ABX56261-ABX56306. 8 296 392 473 154 124 275 LETQAHIQECKHPSVFQHGDNS--FRLLFDVVVILTCSLSFLLCARSLLRGFLLQNEFVG 332 356 STLLVWVGVIRYLTFFHNYNILIATLRVALPSVMRFCCCVAVIYLGYCFCGWIVLGPYHV 452 STLLVWVGVIRYLGYFQAYNVLILTMQASLPKVLRFCACAGMIYLGYTFCGWIVLGPYHD 416 FIALITGAYDTIKHPGGAGAEESELQAYIAQCQDSPTSGKFRRGSGSACSLLCCCGRDP\$ 572 530 and portions of the polynucleotides encoding NOVX polypeptides are useful 96 68 474 FIALITDS/DTIKKFQQNGFPETDLQEFLKECS---SKEEYQKESSAFLSCICCRRRSVS 37 BEEDLRRRLKYFFMSPCDKFRAKGRKPCKLMLQVVKILVVTVQLILFGLSNQLAVTFREE 97 NIIAFRHLFILGYSDGADDTF -- AAYTREQLYQAIFHAVDQYLALPDVSLGRYAYVRGGG 69 NTVAFKHLFLKGYSGTDEDDYSCSVYTQEDAYESIFFAINOYHQLKDITLGTLGY----G 155 DPWTNGSGLALCQRYYHRGHVDPANDTFDIDPMVVTDCIQVDPPERPPPPPSDDLTLLES 215 SSSYKNLTLKFHKLVNVTIHFRLKTINLQSLINNEIPDCYTFSVLITFDNKAHSGRIPIS FMWRQRGRVISLWERLEFVNGWYILLVTSDVLTISGTIMKIGIEAKNLASYDVCSILLGT 417 KPENLNTVAECLFSLVNGDDMFATFA - -QIQQ-KSILVWLFSRLYLYSFISLFIYMILSL KFRSLSMVSECLFSLINGDDMFVTFAAMQAQQGRSSLVWLFSQLYLYSFISLFIYMVLSL Indels 22; Gaps 44.6%; Score 1367; DB 24; Length 544; 49.2%; Pred. No. 1.9e-138; Matches 269; Conservative 112; Mismatches 144; 573 EEHSLLV 579 531 CLFSMLL 537 544 AA; Similarity 393 333 357 513 453 Sequence Query Match Best Local RESULT 10 염 q à 엄 ò g ð Dp ò 셤 8 ò g δ g à à

Tue

12-APR-2001;

gene therapy; dyslipidaemia; cardiomyopathy; metabolic disorder; diabetes; atherosclerosis; obesity; anorexia; neurodegenerative disorder; Alzheimer's disease; cancer; Parkinson's disease; naematopoietic disorder; metabolic disturbance; metabolic syndrome X; wasting disease. antilipaemic; cytostatic; immunomodulatory;

Homo sapiens

WO200281625-A2

03-APR-2002;

2001US-281906P. 2001US-282020P.

2001US-282930P. 2001US-283444P. 2001US-283521P. 2001US-283674P. 2001US-283674P. 2001US-283510P. 2001US-285325P. 2001US-285321P. 2001US-286592P. 2001US-286592P. 17-APR-2001; 20-APR-2001; 13-APR-2001;

24-APR-2001;

2001US-3100883P. 2001US-311003P. 2001US-311973P. 07-JUN-2001; 26-JUN-2001; 08-AUG-2001;

2001US-312901P. 2001US-322283P. 2001US-327448P. 2001US-345734P. .002US-345755P 16-AUG-2001;

(CURA-) CURAGEN CORP.

2002US-0114153

ö Smithson Malyankar UM; u J, Peyman JA; Padigaru M, Shenoy SG, Kekuda R, Rastelli L, Mezes PD, Smi Guo X, Gerlach V, Casman SJ, Boldog FL, Li L, Zerhusen BD Tchernev VT, Gangolli EA, Vernet CAM, Spytek KA, Malyankar Patturajan M, Miller CE, Taupier RJ, Heyes MP, Ju J, Peym Catterton E, MacDougall JR, Edinger SR, Stone DJ, Mazur A,

WPI; 2003-046862/04. N-PSDB; ABX56271.

New isolated NOVX polypeptide useful for treating cardiomyopathy, atherosclerosis, metabolic disorders, diabetes, obesity, infectious disease, anorexia, neurodegenerative disorders, Alzheimer's disease and

Claim 1; Page 110; 425pp; English.

antidiabetic, antiarteriosclerotic, anorectic, metabolic, antimicrobial, neuroprotective, antiparkinsonian, antilipaemic, cytostatic, antimicrobial, neuroprotective, antiparkinsonian, antilipaemic, cytostatic, noctropic, cardiant and immunomodulatory activity. The polypeptide and any antibodies generated from it are useful in the manufacture of a medicament for treating a syndrome associated with a human disease selected from a pathology associated with the NoVX polypeptide. Fragments and portions of the polymuleotides encoding NoVX polypeptides are useful individuals from minute biological samples, as DNA markers for restriction fragment length polymorphism (RFLP), and are useful to prepare polymerses chain reaction primers. The products of the invention disorders, diabetes, atherosclerosis, obesity, infectious disease, anorexia, neurodegenerative disorders, Alzheimer's disease, Parkinson's can be used in gene therapy and for treating cardiomyopathy, metabolic disorders, diabetes, atherosclerosis, obesity infections disease invention describes novel polypeptides, termed NOVX which have

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                  dyslipidaemias, metabolic disturbances associated with obesity, metabolic syndrome syndrome assting disorders associated with chronic diseases and various cancers. ABUI-2041-ABUI-2086 represent the polypeptide fragments encoded by the NoVX polynucleotides represented in ABX56261-ABX56306.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        330 FVGFMWRQRGRVISLWERLEFVNGWYILLVTSDVLTISGTIMKIGIEAKNLASYDVCSIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      290 FLNFFLEKYKRPVCDTDQWEFINGWYVLVIISDLMTIIGSILKMEIKAKNLTNYDLCSIF
                                                                                                                                                                                                               37 BEEDLRRRLKYFFMSPCDKFRAKGRKPCKLMLQVVKILVVTVQLILFGLSNQLAVTFREE
                                                                                                                                                                                                                                              9 KEECLREDLKFYFMSPCEKYRAPRQIPWKLGLQILKIVMVTTQLVRFGLSNQLVVAFKED
                                                                                                                                                                                                                                                                                   97 NTIAFRHLFLLGYSDGADDTF--AAYTREQLYQAIFHAVDQYLALPDVSLGRYAYVRGGG
                                                                                                                                                                                                                                                                                                                    69 hivafkelkelkeysetdeddyscsvyiqedayesiffalnoyhelkdiflegi----e
                                                                                                                                                                                                                                                                                                                                                         155 DPWINGSGLALCORYYHRGHVDPANDIFDIDPMVVTDCIQVDPPERPPPPSDDLTLLES
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                                                                                                                                                                                 Gaps
                                                                                                                                                                                 32;
                                                                                                                                              Length 540;
                                                                                                                                                                               Indels
 disease, immune disorders, haematopoietic disorders,
                                                                                                                                        ch 42.7%; Score 1311; DB 24; I Similarity 48.0%; Pred. No. 2.2e-132; 264; Conservative 110; Mismatches 144;
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ABB72389 standard; Protein; 255 AA. ABB72389; RESULT 11 ABB72389

(first entry) 04-APR-2002

Human, rat; mouse, skin cell, skin wound, cancer, growth defect, developmental defect, inflammatory disease, dermatological, vulnerary, immunomodulator, anti-inflammatory, cytostatic, neuroprotective. Murine protein isolated from skin cells SEQ ID NO: 713.

WO200190357-A1.

29-NOV-2001

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Li PWD,
                          23-MAR-2001; 2001WO-US09231.
                                                23-MAR-2000; 2000US-191637P.
                                                                                                             Adams M,
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                                                                                    (PEKE ) PE CORP NY.
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N-PSDB; ABL15778
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  27-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97 NTIAFRHLFLLGYSDGADDTFAAYTREQLYQAIFHAVDQYLALPDVSLGRYAYVRGGGDP 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WINGSGLALCORYTHRGHVDPANDTFDIDPMVVTDCIQVDPPERPPPPSDDLTLLESSS 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 WANGSALALCORYTHRGHVDPANDTPDIDPRVYTDCIQVDPPDRPPDIPSEDLDFLDGSA 180
                                                                                                                                                                                                                                             isolated from human, mirine and rat skin cell libraries. The sequences can be used in the development of therapeutic agents useful in the treatment of skin disease; including skin wounds, cancer, growth defects, developmental defects and inflammatory diseases. The proteins have important roles in the induction of hair growth, cell proliferation and cell-cell interaction, in maintaining tissue integrity, in wound healing and in modulating immune responses. The present sequence is a polypeptide of the invention.
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                                                                                                                                                                                                                                   present invention provides the protein and coding sequences of cDNAs
                                                                                    Kumble KD;
                                                                                                                                                                                                                                                                                                                                                                                                                              37 BEEDLRRRLKYFFMSPCDKFRAKGRKPCKLMLQVVKILVVTVQLILFGLSNQLAVTFREE
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                                                                                                                                             New polynucleotides and polypeptides encoded by the polynucleotides isolated from skin cells, useful for treating skin wounds, cancers, growth and developmental defects, inflammatory diseases, or for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila; developmental biology; cell signalling; insecticide;
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                                                                                    Murison JG,
                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                               40.0%; Score 1226; DB 23;
89.7%; Pred. No. 1.1e-123;
tive 13; Mismatches 13;
                                                                                    Onrust R,
                                                                                    Sleeman M,
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                                                             (GENE-) GENESIS RES & DEV CORP LID
                                                                                                                                                                                                            Claim 4; Page 455; 466pp; English.
                        24-MAY-2000; 2000US-206650P.
25-JUL-2000; 2000US-221232P.
 24-MAY-2001; 2001WO-NZ00099
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                                                                                                                                                                                                                                                                                                                                                                                                      Matches 227; Conservative
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                                                                                    Strachan L,
                                                                                                             WPI; 2002-122020/16
                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                          N-PSDB; ABL35079
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                                                                                    Watson JD,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   328 NEFVGFMWRQRGRVISLWERLEFVNGWYILLVTSDVLTISGTIMKIGIEAKNLA--SYDV 385
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ω
                                                                                                                                                                                                                                            New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or mare genes from Drosophilar. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical dargs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01861-0-ABL30512).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    263 NYLRORDVEVNPASLVSAQLTFKIKTVNFKA--NGGPLSAPDCFRFDISITFNNRDHDGQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure, SEQ ID NO 41817; 21pp + Sequence Listing; English
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Myers EW,
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Tue Oct 28 16:50:37 2003

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Best Local Similarity
                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags of for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving antibodies against it, detecting or (II). (II) is useful for generating antibodies against it, detecting or ganditating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (II) and (II) are useful for treating associaters involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutuations or responsible for genetic disorders or other traits to assess biodiversity and in the polypeptide and polymucleotide sequences have applications in the polypeptide and polymucleotide sequences have applications in the polypeptide and polymucleotides of the context o
                                                 -----RRG 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and to produce other types of data and products dependent on DNA and amino acid sequences. ABG30010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; chromosome mapping; gene mapping; gene therapy, forensic, food supplement; medical imaging; diagnostic; genetic disorder.
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                  IYMVLSLFIALITGAYDTIKHPGGAGAEESELQAYI-AQCQDSPTSGKF-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 20; SEQ ID No 32103; 103pp; English.
                                                                                                                                                     FLDVVKSICCCGRCGRHQEPAQPNS 642
                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel human diagnostic protein #1735.
                                                                                                                      SGSACSLLCCCGR----DPSEEHS
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23-AUG-2000; 2000US-0649167.
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N-PSDB; AAS65931.
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                                          1 MTAPAGPRGSETERLLTPNPGYGTQAGPSPAPPTPPEEEDLRRRLKYFFMSPCDKFRAKG
                                                                1 MTAPAGPRGSETERFLTPNPGYGTQAGPSPAPPTPPEEEDLRRRLKYFFWSPCDXFRAKG
                                                                                   61 RKPCKLMLQVVKILVVTVQLILFGLSNQLAVTFREENTIAFRHLFLLGYSDGADDTFAAY
                                                                                                                                                                                                                                                                                                                              Human, TANGO 315, clone jthkal73a09, TANGO 330, TANGO 437, TANGO 480, cellular process regulator, gene therapy, keratinocyte disorder, squamous cell carcinoma, keratitis.
                         Gaps
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/mote= "Alternatively this residue is Lys due to
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                        Indels
Pred. No. 3.9e-97;
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/label= Mature_TANGO_480_protein
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/label= Extracellular_domain
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/label= Transmembrane_domain
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/note= "Alternatively this
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/label= Cytoplasmic_domain
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            98.4%;
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                       183; Conservative
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The present sequence representing human TANGO 480 is isolated from CDNA clone jthka173a09 from a human keratinocyte cDNA library.

TANGO 480 is 1 of 4 movel human transmembrane proteins which also includes TANGO 315 (AAU00499-AAU00503) (AAU00500-AAU00501),

TANGO 417 (AAU00502). The nucleic acids encoding these proteins an adulating agents in regulating a variety of cellular processes and can be used to express the proteins in a host cell in gene therapy applications. Antisense nucleic acids are also described. Signostic assays can be used to detect genetic alterations in the TANGO nucleic acids and to identify compounds that bind to or modulate activity of nucleic acids and to identify compounds that bind to or modulate activity contint protein levels in tissue as a clinical testing procedure.

TANGO 480 nucleic acids and proteins may be used to diagnose, treat and monitor keratinocyte disorders e.g. squamous cell carcinoma, keratitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   299 LLFDVVVILTCSLSFLLCARSLLRGFLLQNBFVGFMWRQRGRVISLWERLEFVNGWYILL 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                359 VTSDVLTISGTIMKIGIEAKNLASYDVCSILLGTSTLLVWVGVIRYLTFFHNYNILIATL 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 IISDILTIIGSILKMEIQAKSLTSYDVCSILLGTSTMLVWLGVIRYLGFFAKYNLLILTI 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               419 RVALPSVMRFCCCVAVIYLGYCPCGWIVLGPYHVKFRSLSMVSECLFSLINGDDMFVTFA 478
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                                                                                                                                                                                                                                                                                Isolated secreted proteins and their encoding nucleic acids are use for diagnosis and treatment of e.g. bacterial and viral infections,
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                                                                                                                                                                                                                                                                                                                    autoimmune diseases and inflammatory disorders -
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                                                                                                                                                                              Kirst S, Wrighton N, Fraser CC;
                                                                                                                                                                                                                                                                                                                                                               Claim 9; Fig 22; 261pp; English.
                                                                                                                                        (MILL-) MILLENNIUM PHARM INC.
                                                           02-OCT-2000; 2000WO-US27202.
                                                                                             99US-0409634
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                                                                                                                                                                                                                    2001-235372/24.
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                                                                                                 30-SEP-1999;
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                     05-APR-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to novel genes (ABL89449-ABL90853) and proteins (ABB89040-ABB90444) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital, (b) immune disorders e.g. Addison's disease, allergies, autoimmune historiation and preventics and ulcerative disease, multiple sclerosis, rheumatonia architis and ulcerative colitis, (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
                                                                                                                                                                                                                                                                                                                                                                                                          Novel 1405 isolated polypeptides, useful for diagnosis, treatment and prevention of neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            334 MWRQRGRVISLWERLEFVNGWYILLVTSDVLTISGTIMKIGIEAKNLASYDVCSILLGTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   394 TLLVWVGVIRYLTFFHNYNILIATLRVALBSVMRFCCCVAVIYLGYCFCGWIVLGPYHVK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 11; SEQ ID NO 1666; 2081pp + Sequence Listing; English
neurological disease; infection; human; secreted protein
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                                                                                                                                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                     18-MAY-2001; 2001WO-US16450
                                                                                                                                                                                                              19-MAY-2000; 2000US-205515P
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                                                                                                                                                                                                                                                                                                       Rosen CA;
                                                                                                                                                                                                                                                                                                                                              WPI; 2002-122018/16.
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                                           Homo sapiens.
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| cgn2 6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
| cgn2 6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
| cgn2 6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
| cgn2 6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
| cgn2 6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
| cgn2 6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
| cgn2 6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
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| cgn2 6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
| cgn2 6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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US-10-184-644-332
US-10-184-634-332
US-10-184-634-332
US-10-101-487-106
US-09-953-348-9
US-10-267-255-9
US-09-953-348-9
US-09-953-348-9
US-09-953-348-76
US-09-476-242-24
US-09-476-242-24
US-09-476-242-18
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US-09-828-466-3
; Sequence 3, Application US/09828466
; Perent No. US2002003505A1
; GENERAL INPORMATION:
; APPLICANT: Curtis, Rory A.J.;
APPLICANT: Silos-Santiago, Immaculada
ITLE OF INVENTOR: 54420, A NOVEL HUMAN CALCIUM CHANNEL
; TILE REFREENCE: MNI-125CP
; CURRENT FILING DATE: 2001-04-06
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 09/544,797
; RIGHER FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin Ver. 2.0
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Best Local Similarity 100.0%; Pred. No. 1.1e-298;
Matches 1101; Conservative 0; Mismatches 0;
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LENGTH: 1740
TYPE: DNA
ORGANISM: Homo sapiens
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100.0%; Score 1101; DB 13;
Best Local Similarity 100.0%; Pred. No. 1.1e-298;
Matches 1101; Conservative 0; Mismatches 0;
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                            NAME/KEY: CDS
; LOCATION: (1)..(1740)
US-10-103-458-3
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Publication No. US20020197680A1
GENERAL INFORMATION:
APPLICANT: Curtis, Rory A.J.
TITLE OF INVENTION: 54420, A NOVEL HUMAN CALCIUM CHANNEL
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| | ATCHACACACACACGGGGGGGCCCTGCCCAGCGTCATGCGCTTCTGCTGCTGCGCGCACACCTGCCGGGGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTG | | ORGANIAN ORGANIAN | 0 61 GAGCGGATGACCTTCGCAGCTACACGGGAGCACTGTACCAGGCCATCTTCCATG 120 11 11 11 11 11 11 1 |

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US-09-820-833-26
| Gequence 26, Application US/09820893
| Patent No. US20020076705A1
| GENERAL INFORMATION:
| APPLICANT: Rosen et al.;
| TILLE OF INVENTION: 31 Human Secreted Proteins;
| FILE REPREDICE: PZ033P1
| CURRENT FILING DATE: 2001-03-30
| PRIOR APPLICATION NUMBER: 09/531,119
| PRIOR PILING DATE: 2000-03-20
| PRIOR APPLICATION NUMBER: 60/102,895
| PRIOR PILING DATE: 1998-10-02
| NUMBER: OF SEQ ID NOS: 1400
| SOSTWARR: Patentin Ver. 2.0
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Best Local Similarity 99.8
Matches 1099; Conservative
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ORGANISM: Homo sapiens
FEATURE:
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                                                                                                     Query Match
100.0%; Score 1101; DB 13; Length 2095;
Best Local Similarity 100.0%; Pred. No. 1.2e-298;
Matches 1101; Conservative 0; Mismatches 0; Indels 0;
                                 ; NAME/KEY: CDS
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US-10-103-458-1
ORGANISM: Homo sapiens
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US-09-965-529-50
is Sequence 50, Application US/09965529
publication No. US20020182671A1
GENERAL INPORMATION:
APPLICANT: LAL, Preeti
APPLICANT: TANG, Y. Tom
APPLICANT: BADDWAN, Olga
APPLICANT: BADDWAN, Olga
APPLICANT: BAUGHN, Mariah R.
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APPLICANT: DATTERSON, Chandra
ITILE OF INVENTION: MEMBRANE ASSOCIATED PROTEINS
ITILE OF INVENTION WINBER: US/09/965,529
CURRENT APPLICATION NUMBER: 60/149,641; 60/164,203; PCT/US00/22315
PRIOR FILING DATE: 1999-08-17; 1999-11-09; 2000-08-14
SOFTWARE: PROGRAM
SEQ ID NOS: 74
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TYPE: DNA
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                        CCATCCACTTCCGGCTGAAGACCATTAACCTCCAGAGCCTCATCAATAATGAGATCCCGG
TGGAAAGCAGCTCCAGTTACAAGAACCTCACGACTAAATTCCACAAGCTGGTCAATGTCA
                                                                                 CCATCCACTTCCGGCTGAAGACCATTAACCTCCAGAGCCTCATCAATAATGAGATCCCGG
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GENERAL INFORMATION:
APPLICANT: Strachan, Lorna
APPLICANT: Steaman, Matthew
APPLICANT: Orlust, Rene
APPLICANT: Only Krishanand D.
APPLICANT: Munison, James G.
APPLICANT: Munison, James G.
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods for Their Use
FILE REPERENCE: 11000.1011c4U
CURRENT APPLICATION NUMBER: US/09/866,050A
CURRENT FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 725
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 608-850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 608, Application US/09866050A; Publication No. US20030040471A1 ; GENERAL INFORMATION:
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                                         ATATCCTCATCGCCACACTGCGGGTGGCCCTGCCCAGCGTCATGCGCTTCTGCTGCCG
               ATATCCTCATCGCCACACTGCGGGTGGCCCTGCCCAGCGTCATGCGCTTCTGCTGCTGCTGCG
                                                                                                TGGCTGTCATCTACCTGGCTACTGCTTCTGTGGATCGTGGGGGCCCTATCATG
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; NAME/KEY: misc_feature

; OTHER INFORMATION: Incyte ID No. US20030124649A1 977658CB1

US-09-969-680A-50
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99.9%; Score 1099.4; DB 11;
Best Local Similarity 99.9%; Pred. No. 3.4e-298;
Matches 1100; Conservative 0; Mismatches 1; I
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APPLICANT: LAL, Preeti; YUE, Henry
APPLICANT: LAL, Preeti; YUE, Henry
APPLICANT: BURFORD, Neil; AZIMZAI, Yalda
APPLICANT: BURFORD, Neil; LAZIMZAI, Yalda
APPLICANT: BAUGHN, MATIBAB, LU, Dyung Aina M.
APPLICANT: PATTERSON, Chandra
TITLE OF INVENTION: MEMBRENE ASSOCIATED PROTEINS
FILE REFERENCE: PF-0731-1 USA
CURRENT PILING DATE: 2001-10-02
PRIOR PELICATION NUMBER: USO0/22315
PRIOR PELICATION NUMBER: 60/149,641
PRIOR PELICATION NUMBER: 60/149,641
PRIOR PELICATION NUMBER: 60/14,203
PRIOR PELICATION NUMBER: 60/164,203
PRIOR PILING DATE: 1999-08-17
PRIOR PILING DATE: 1999-08-17
PRIOR PILING DATE: 1999-08-17
SPRIOR PILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 74
SOFTWARE: PERL PROGRAM
                                                                                                                                                                                                                TGAAGTTCCGCTCACTCCCA 1482
                                                                                                                                                                                 TGAAGTICCGCTCACTCCCA 1101
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ORGANISM: Homo sapiens
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                                                                                          TGGCTGTCATCTACCTGGGCTACTGCTTCTGTGGCTGGATCGTGCTGGGGCCCTATCATG 1080
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APPLICANT: Strachan, Lorna
APPLICANT: Strachan, Lorna
APPLICANT: Strachan, Lorna
APPLICANT: Steeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Munison, James G.
APPLICANT: Munison, James G.
APPLICANT: Munble, Krishanand D.
TITLE OF INVENTION: Compositions isolated From Skin Cells
TITLE OF INVENTION NUMBER: 05/20,152,661
CURRENT APPLICATION NUMBER: 06/221,232
PRIOR FILING DATE: 2000-07-25
PRIOR FILING DATE: 1999-04-29
PRIOR FILING DATE: 1999-04-29
PRIOR FILING DATE: 1999-11-09
PRIOR APPLICATION NUMBER: 09/188,930
PRIOR FILING DATE: 1999-04-29
PRIOR FILING DATE: 1999-04-29
PRIOR FILING DATE: 1998-11-09
PRIOR FILING DATE: 1998-11-09
PRIOR FILING DATE: 1998-04-29
NUMBER OF SEQ ID NOS: 725
SOFTWARE: FASLSEQ for Windows Version 4.0
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85.8%; Pred. No. 1.2e-228;
ive 0; Mismatches 156;
                                                                                                                                                                                                     TGAAGTTCCGCTCACTCTCCA 1101
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                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 608, Application US/10152661
; Publication No. US20030022835A1
; GENERAL INFORMATION:
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Best Local Similarity 85.8
Matches 945; Conservative
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                                                                                                                Score 851.4; DB 11; Length 1827;
Pred. No. 1.2e-228;
0; Mismatches 156; Indels 0;
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                                                                                                             77.3%;
Similarity 85.8%;
5; Conservative 0
TYPE: DNA
ORGANISM: Mouse
                                                        US-09-866-050A-608
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Best Local Simi
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Pred. No. 5.1e-47;
0; Mismatches 177;
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NR APPLICATION UNMER: 09/630,334
OR FILING DATE: 2000-07-31
OR APPLICATION NUMBER: 09/606,565
    R APPLICATION NUMBER: 09/224,246
R FILING DATE: 1998-12-30
R APPLICATION NUMBER: 09/259,388
R FILING DATE: 1999-02-26
R APPLICATION NUMBER: 60/122,458
R APPLICATION NUMBER: 09/312,359
R FILING DATE: 1999-03-01
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APPLICATION NUMBER: 09/336,536
FILING DATE: 1999-04 17
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APPLICATION NUMBER: 00/7
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FILING DATE: 1999-12-29
APPLICATION NUMBER: 09/514,010
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FILING DATE: 1999-12-29
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  PRIOR APPLICATION NUMBER: 09/224
PRIOR PILING DATE: 1999-12-30
PRIOR PILING DATE: 1999-02-05
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Best Local Similarity 63.7%;
Matches 310; Conservative
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; ORGANISM: Homo sapiens
US-09-796-753-161
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| Publication No. US20030027998A1
| GENERAL INFORMATION:
| APPLICATION No. US20030027998A1
| TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
| FILE REFERENCE: 7853-227-999
| CURRENT APPLICATION NUMBER: US/09/796,753
| CURRENT FILING DATE: 2001-03-01
| PRIOR APPLICATION NUMBER: 09/183,175
| PRIOR APPLICATION NUMBER: 09/183,175
| PRIOR PELING DATE: 1998-12-30
| PRIOR FILING DATE: 1998-12-30
| PRIOR APPLICATION NUMBER: 09/223,546
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PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/283710
PRIOR FILING DATE: 2001-04-13
PRIOR PPLICATION NUMBER: 60/283678
PRIOR PILING DATE: 2001-04-13
PRIOR PILING DATE: 2001-04-13
PRIOR PILING DATE: 2001-04-17
Prior Application data removed - See File Wrapper of the Prior Proposition of the Prior Prior
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LOCATION: (31)..(1663)
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US-10-114-153-27
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LENGTH: 16
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TITLE OF INVENTION: NOVEL ANTIBODIES THAT BIND TO ANTIGENIC POLYPEPTIDES, NUCLEIC ACT
TITLE OF INVENTION: BNCODING THE ANTIGENS, AND METHODS OF USE
TITLE OF INVENTION: ENCODING THE ANTIGENS, AND METHODS OF USE
FILE REFERENCE: 21402-322A
CURRENT APPLICATION NUMBER: US/10/114,153
FRIOR APPLICATION NUMBER: 60/28196
PRIOR APPLICATION NUMBER: 60/28196
PRIOR PLING DATE: 2001-04-05
PRIOR PLING DATE: 2001-04-06
PRIOR FILING DATE: 2001-04-06
PRIOR PLING DATE: 2001-04-10
PRIOR PLING DATE: 2001-04-10
PRIOR PLING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/28314
PRIOR PLING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/28344
                                                                                                                                                                                                                                                                                                             975 ACACTGCGGGTGGCCCTGCCCAGCGTCATGCGCTTCTGCTGCTGCTGCTGTCATCTAC 1034
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                                      GCCAAGAACTIGGCGAGCTACGACGICTGCAGCAICCTCGGGCACCTCGAGGCGTGCTG 914
                                                                                                   280 deraagagreraacragrrangargrergraggaracrictrogggaerreraccargerr 339
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Spytek, Kimberly
Malyankar, Uriel
Patturajan, Meera
Miller, Charles
Taupier, Raymond Jur.
Heyes, Melvyn
Ju, Jingfang
Peyman, John
Catterton, Elina
MacDougall, John
Edinger, Shlomit
Stone, David
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Publication No. US20030185815A1
GENERAL INFORMATION:
APPLICANT: Padigaru, Muralidhara
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Rekuda, Ramesh
Rastelli, Luca
Mazes, Peter
Smithson, Glennda
Guo, Xiaojia
Gerlach, Valerie
Casman, Stacie
Boldog, Ferenc
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Tchernev, Velizar
Gangolli, Esha
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            722 CTTCAGACTGGAATTTTATCGGCTCTTACAGGTTGAAATCTCCTTTCATCTTAAAGGCAT 781
                                                                                                                                                                                                                                                                                                                                                                                 902 AATTGAAGAATGTAAAGACTTGAACATATTTGGATCAGCTCAGAAAATGCTCAGTATGT
                                                                            446 TAACCTCCAGAGCCTCATCAATAATGAGATCCCGGACTGCTATACCTTCAGCGTCCTGAT
                                                                                                                                                                                               506 CACGITIGACAACAAAGCACACAGTGGGCGGATCCCCCATCAGCCTGGAGACCCAGGCCCA
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Publication No. US20030185815A1
GENERAL INFORMATION:
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Shenoy, Suresh
Kekuda, Ramesh
Rastelli, Luca
Mezes, Peter
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Gangolli, Esha
Vernet, Corine
Spytek, Kimberly
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Gerlach, Valerie
Casman, Stacie
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Taupier, Raymond
Heyes, Melvyn
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US-10-114-153-25
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PRIOR PILING DATE: 2001-04-12
PRIOR PILING DATE: 2001-04-12
PRIOR PILING DATE: 2001-04-12
PRIOR PILING DATE: 2001-04-12
PRIOR PILING DATE: 2001-04-13
PRIOR PILING DATE: 2001-04-17
Sequence 27, Application US/10114153
Publication No. US20030185815A1
GENERAL INFORMATION:
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IOR APPLICATION NUMBER: 60/282930
IOR FILING DATE: 2001-04-10
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PRIOR FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 60/282020
                                                                                  APPLICANT: Padigaru, Muralidhara
                                                                                                                         Shenoy, Suresh
Kekuda, Ramesh
Rastelli, Duca
Mezes, Peter
Smithson, Glennda
Guo, Xiaojia
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Tchernev, Velizar
Gangolli, Esha
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Edinger, Shlomit
Stone, David
Mazur, Ann
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Patturajan, Meera
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Taupier, Raymond
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Casman, Stacie
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Catterton, Elina
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Ju, Jingfang
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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (93)..(1791)
US-10-114-153-27
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1056 GAATCÍCACAAACTATGATCÍCTGCAGCATTÍTCTTGGAACCÍCTAGGCTCTTGGTTTG 1115
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936 CAAGCGGCCTGTGTGTGACACCGACCAGTGGGAGTTCATCAACGGCTGGTATGTCCTGGT 995
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APPLICANT: Millet, Isabelle
APPLICANT: Millet, Isabelle
TITLE OF INVENTION: ANTISENSE MODULATION OF PROTEIN EXPRESSION
CURRENT APPLICATION NUMBER: US/10/305,810
CURRENT FILING DATE: 2002-11-27
PRIOR PILING DATE: 2001-12-29
PRIOR PILING DATE: 2001-12-29
PRIOR PILING DATE: 2001-12-29
PRIOR FILING DATE: 2001-20-4
PRIOR PILING DATE: 2000-07-26
PRIOR PILING DATE: 2000-07-26
PRIOR PILING DATE: 2000-03-39
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-09-19
PRIOR PILING DATE: 2000-09-19
PRIOR PILING DATE: 2001-10-09-19
PRIOR PILING DATE: 2001-10-09-19
PRIOR PILING DATE: 2001-10-09-19
PRIOR PILING DATE: 2001-10-04
PRIOR PILING DATE: 2000-02-15
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Simons, Jan Fredrik
Tailon, Bruce E.
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Peyman, John A.
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Best Local Similarity 56.3
Matches 388; Conservative
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                                                                                                                                                                                                                                                                                           APPLICANT: Stone, bavid
APPLICANT: Mazur, Ann
TITLE OF INVENTION: NOVEL ANTIBODIES THAT BIND TO ANTIGENIC POLYPEPTIDES, NUCLEIC ACT
TITLE OF INVENTION: ENCODING THE ANTIGENS, AND METHODS OF USE
FILE REFERENCE: 21402-322A
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0; Mismatches 304; Indels 6;
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PRIOR APPLICATION NUMBER: 60/28200
PRIOR PILICATION NUMBER: 60/28200
PRIOR PILICATION NUMBER: 60/28230
PRIOR FILING DATE: 2001-04-10
PRIOR PILICATION NUMBER: 60/283512
PRIOR PILICATION NUMBER: 60/283512
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PRIOR
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PRIOR APPLICATION NUMBER: 60/281086
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Best Local Similarity 56.2%;
Matches 398; Conservative C
                                                                                                                                                                     MacDougall, John
Edinger, Shlomit
Stone, David
Mazur, Ann
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TITLE OF INVENTION: NOVEL ANTIBODIES THAT BIND TO ANTIGENIC POLYPEPTIDES, NUCLEIC ACTIVE OF INVENTION: BACODING THE ANTIGENS, AND METHODS OF USE
TITLE OF INVENTION: ENCODING THE ANTIGENS, AND METHODS OF USE
CURRENT APPLICATION NUMBER: US/10/114,153
CURRENT FILING DATE: 2002-08-06
FRIOR FILING DATE: 2001-04-03
FRIOR APPLICATION NUMBER: 60/281086
FRIOR FILING DATE: 2001-04-03
FRIOR APPLICATION NUMBER: 60/28200
FRIOR APPLICATION NUMBER: 60/28200
FRIOR FILING DATE: 2001-04-10
FRIOR FILING DATE: 2001-04-10
FRIOR FILING DATE: 2001-04-12
FRIOR PELING DATE: 2001-04-12
FRIOR APPLICATION NUMBER: 60/28344
FRIOR FILING DATE: 2001-04-13
FRIOR PELING DATE: 2001-04-13
FRIOR PELING DATE: 2001-04-13
FRIOR FILING DATE: 2001-04-17
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Miller, Charles
                     Taupier, Raymor
Heyes, Melvyn
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Best Local Simi
Matches 388;
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                  TICCACAAGCIGGICAAIGICACCAICCACTICCGGCIGAAGACCAITAACCICCAGAGC 458
                                                                   Trantcaggerenacaggineaaaneneenenteaaaggerinaaaggeatigaeenagaea 645
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Publication No. US20030185815A1
GENERAL INFORMATION:
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APPLICANT: Shenoy, Suresh
APPLICANT: Rekuda, Ramesh
APPLICANT: Rastelli, Luca
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Zerhusen, Bryan
Tchernev, Velizar
Gangolli, Esha
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Spytek, Kimberly
Malyankar, Uriel
Patturajan, Meera
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Guo, Xiaojia
Gerlach, Valerie
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Boldog, Ferenc
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819 ACCATCTCGGGCACCATCATGAAGATCGGCGATCGAGGGCCAAGAACTTGGCGAGCTACGAC 878
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DNA encoding novel
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AAS72274 ABL89699

AAI61022

Human TANGO 480 cD Human NOV9b CG9070 Human NOV9d CG9070 Human NOV9c CG9070 Human NOV9a CG9070 Human immune/haema

DNA encoding

AAS65933

AAH14814

Drosophila melanog Human secreted pro DNA encoding novel Drosophila melanog

Human immune/haema

AAK73826 ABL29717 ABA08523

AAK73827

ABX56271

AAS89310 ABL29716 AAK58837

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Transient receptor potential like calcium channel; TRP; TLCC-2; human; neuroprotective; analgesic; nootropic; antiparkinsonian; antidepressant; cerebroprotective; anxiolytic; antimanic; anticonvulsant; gene therapy; calcium signaling; gene; ss.
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/product= "TLCC-2"
/note= "transient receptor potential-like calcium
channel"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1740 BP; 319 A; 578 C; 475 G; 368 T; 0 other;
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nes 1101; Conservative
                        CURTIS R A J.
SILOS-SANTIAGO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to the protein and coding sequences of human transient receptor potential (TRP)-like calcium channel protein-2 (TLCC-2). The sequences can be used in the treatment of TLCC-2 related disorders, including central nervous system disorders such as Alzheimer's, Parkinson's and Huntington's diseases, multiple sclerosis, falles de la Tourette's syndrome, autonomic function disorders, learning or memory disorders, pain disorders and disorders of cellular proliferation, including cancer. The present sequence is the TLCC-2
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                                                                                                                                                                                                                                                                                                                                  Novel isolated human transient receptor potential-like calcium channel protein-2 useful for treating Alzheimer's disease, depression, amnesia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CATTCCGGGAAGAGAACACCATCGCCTTCCGACACCTCTTCCTGCTGGGCTACTCGGACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seguence 1740 BP; 319 A; 578 C; 475 G; 368 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Fig 1; 148pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
                                                                                               Silos-Santiago
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pain disorder, and cancer -
(MILL-) MILLENIUM PHARM INC
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Matches 1101; Conservative
                                                                                                                                                                                               WPI; 2002-010913/01
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nociception, nootropic; neuroprotective, antiparkinsonian; cytostatic; hypotensive, antidepressant; analgesic; anticonvulsant; tranquiliser; Parkinson's disease; Huntington's disease; multiple sclerosis; Gilles de la Tourette's syndrome; autonomic function disorder; cancer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; TLCC-2; TRP-like calcium channel; membrane excitability;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         neuroleptic; gene therapy; Alzheimer's disease; CNS disorder;
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                                                                                                                                                                                                            The invention relates to a novel transient receptor potential (TRP)-like calcium channel, designated TLCC-2 and polymucleotides encoding the TLCC-2. TLCC-2 can be expressed by standard recombinant methodology. The TLCC-2 polypeptide, polymucleotides and modulators are useful for treating central nervous system disorders such as neurodegenerative disorders for example Alzheimer's disease, Parkinson's disease, multiple sclerosis, amyotrophic lateral sclerosis, progressive supranuclear palsy, epilepssy, Creutzfeldt-Jakob disease, AIDS-related dementia, familial infantile convulsions, paroxysmal chorocathetosis, psychoses, mania or phobic such as depression, anxiety, schizophrenia, psychoses, main or phobic memory loss, or a neurological disorder such as amnesia, age-related memory loss, or a neurological disorder. Such as migraine. The molecules are also useful to treat a pain disorder. Such as migraine. The molecules are DNA encoding the human TLCC-2 polypeptide.
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                                                                                                                       disorders, including central nervous system disorders such as Alzheimer's, Parkinson's and Huntington's diseases, multiple sclerosis, Gilles de la Tourette's syndrome, autonomic function disorders, learning or memory disorders, pain disorders and disorders of cellular proliferation, including cancer. The present sequence is the TLCC-2 coding sequence including the 3' UTR.
                                                                                                                                                                                                                                                                                                                              9
                                                                           The present invention relates to the protein and coding sequences of human transient receptor potential (TRP)-like calcium channel protein-2 (TLCC-2). The sequences can be used in the treatment of TLCC-2 related
 protein-2 useful for treating Alzheimer's disease, depression, amnesia
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                                                                                                                                                                                                                                                            Score 1101; DB 24;
Pred. No. 1.9e-239;
0; Mismatches 0;
                                               Claim 1, Fig 1, 148pp; English
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100.0%;
                   pain disorder, and cancer
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Best Local Similarity 100.
Matches 1101; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to novel genes (ABL89449-ABL90853) and proteins (ABB89040-ABB90444) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
                     1195 ATGGCTGGTACATCCTGCTCGTCACCAGCGATGTGCTCACCATCTCGGGCACCATCATGA
                                                                                                                                1255 AGATCGGCATCGAGGCCAAGAACTTGGCGAGCTACGACGACGTCTGCAGCATCCTCGGGCA
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ATGCCTGCTACATCCTGCTCGTCACCAGCGATGTGCTCACCATCTCGGGCACCATCATGA
                                                                                         AGATCGGCATCGAGGCCAAGAACTTGGCGAGCTACGACGTCTGCAGCATCCTCGGGCA
                                                                                                                                                                                        CCTCGACGCTGCTGGTGTGGGTGGCGTGATCCGCTACCTGACCTTCTTCCACACTACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prevention of neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for diagnosis, treatment
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TGGCTGTCATCTACTGGGCTACTGCTTCTGTGGCTGGATCGTGCTGGGGCCCTATCATG 1080
                                                                                                                                                                                                                        expressed in. Examples of the activities are: cytostatic, and vulnerary. The anti-proliferative; immunosuppressive; antibacterial; and vulnerary. The secreted proteins and their related polynucleotide sequences are useful for diagnostic and therapeutic methods useful for diagnostic and therapeutic methods useful for diagnosing and treating disorders related to the secreted proteins. The proteins, and polynucleotide sequences may be useful for treating disorders of the immune system, hyperproliferative disorders, infectious disease, regeneration of tissues, for chemotaxis and for screening molecules that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; secreted protein; cytostatic; anti-proliferative; vulnerary; immunosuppressive; antibacterial; diagnosis; immune system; chemotaxis; hyperproliferative disorder; infectious disease; tissue regeneration; screening; food additive; preservative; wound healing;
                           AGATCGGCATCGAGGCCAAGAACTTGGCGAGCTACGACGTCTGCAGCATCCTCCTGGGCA
                                                                                                                                                             ATATCCTCATCGCCACACTGCGGGTGGCCCTGCCCAGCGTCATGCGCTTCTGCTGCTGCTGCG
                                                                                                     961 ATATCCTCATCGCCACACTGCGGGTGGCCCTGCCCAGCGTCATGCGCTTCTGCTGCTGCG
                                                                        CCTCGACGCTGCTGGTGGGTGGGCGTGATCCGCTACCTGACCTTCCTCCACAACTACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The polynucleotide sequences given in AAA39052 to AAA39088 encode the human secreted proteins given in AAB08891 to AAB08984. The human secreproteins can have activities based on the tissues and cells they are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human secreted proteins and coding sequences useful in diagnostic therapeutic methods for disorders such as immune system or proliferative disorders, related to the proteins
        AGATCGGCATCGAGGCCAAGAACTTGGCGAGCTACGACGTCTGCAGCATCCT
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ss GA, Soppet DR;
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                                                                                                                                                                                                                                                                   TGAAGTTCCGCTCACTCTCCA 1101
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P-PSDB; AAB08906.
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               haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis, (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections.
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                                                                                                              Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTGGGGGTGACCCTTGGACCAATGGCTCAGGGCTTGCTCTCTGCCAGCGGTACTACCACC
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     allergies, autoimmune
                                                                                                                                                                                                                  DB 24; Length 2092;
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                                                                                                                                                                                                                                                Indels
                                                                                                                                                                              Sequence 2092 BP; 399 A; 676 C; 590 G; 425 T; 2 other;
                                                                                                                                                                                                              ; Score 1100.6; DB 2
Pred. No. 2.4e-239;
1; Mismatches 0;
   disease,
immune disorders e.g. Addison's
                                                                                                                                                                                                                100.0%;
                                                                                                                                                                                                                               99.66;
                                                                                                                                                                                                                                              Conservative
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Best Local Similarity
Matches 1100; Conserv
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                                                              antagonists of the proteins may be used to prevent scar tissue growth during wound healing, and hyper-vascular diseases. AAA39043 to AAA39051 and AAB08890 are sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAGGCCACGTGGCCCAACGACACATTTGACATTGATCGATGGTGGTTACTGACT
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   ре
                                                                                                                                                                                                               Gaps
                  used as food additives or preservatives, to increase or decrease st capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, co-factors or other nutritional components. Agonists or
   polynucleotide sequences may
                                                                                                                                                                            99.9%; Score 1100.2; DB 21; Length 2094; 99.8%; Pred. No. 2.9e-239;
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0
                                                                                              are sequences used in the exemplification of
                                                                                                                                                                                                             Indels
                                                                                                                                              BP; 400 A; 673 C; 589 G; 426 T; 6 other;
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                                                                                                                                                                                                           2; Mismatches
   proteins or
   The
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   proteins.
                                                                                                                                                                                            Similarity
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Matches 1099;
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1222 AGATCGGCATCGAGGCCAAGAACTTGGCGAGCTACGACGTCTGCAGCATCCTCCTGGGCA 1281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seguence
                                                                                                                                                                                        1402 IGGCTGTCATCTACCTGGCCTACTCCTTCTGTGGCTTGGATCGTGCTGGGGCCCCTATCATG
                                                                   1282 CCTCGACGCTGCTGGTGTGGGTGGGCGTGATCCGCTACCTGACCTTCTTCCACAACTACA
                                                                                                     ATATCCTCATCGCCACACACTGCGGGTGGCCCTGCCCAGCGTCATGCGCTTCTGCTGCTGCT
                                                                                                                                   1342 ATATCCTCATCGCCACACACTGCGGGTGGCCCTGCCCAGCGTCATGCGCTTCTGCTGCTGCG
                                                                                                                                                                     TGGCTGTCATCTACCTGGGCTACTGCTTCTGTGGCTGGATCGTGCTGGGGCCCTATCATG
                                 CCTCGACGCTGCTGCTGTGGGGTGGGCGTGATCCGCTACCTGACCTTCTTCCACAACTACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antiinflammatory; anticonvulsant; immunosuppressive; antidiarrheic; antiarterioscelerotic; gene therapy; cell proliferative disorder; autoimmune disorder; inflammatory disorder; neurological disorder; gastrointestinal disorder; cancer; inflammation; atherosclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; membrane associated protein; MEMAP; diagnosis; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isolated polypeptide with a human membrane associated protein
is useful for the diagnosis, prevention and treatment of cell
proliferative, autoimmune/inflammatory, neurological and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ×
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rson C;
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R, Lu DAM,
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             MEMAP proteins can be used to screen for compounds which specifically bind MEMAP including antibodies, oligonucleotides, proteins and small molecules. MEMAP polynucleotides can be used to prepare transgenic animals which can be studied to provide information concerning human disease. Anti-MEMAP antibodies are useful in immunoassays for the detection of MEMAP protein and can be used as antagonists to treat or prevent a disorder associated with MEMAP. Polynucleotides encoding MEMAP can be delivered to target calls with genetic abnormalities with respect to the expression of MEMAP to treat or prevent a disorder associated
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 cancer, inflammation, atherosclerosis, epilepsy and diarrhoea
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                                                                                                                                                                                              Sequence 2052 BP; 375 A; 670 C; 582 G; 425 T; 0 other;
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Pred. No. 4.4e-239;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-brager Syndrom; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                AGATCGGCATCGAGGCCAAGAACTTGGCGAGCTACGACGTCTGCAGCATCCTCCTGGGCA
                                                                                                                                        CCTCGACGCTGCTGGTGGGTGGGCGGATCCGCTACCTGACCTTCTTCCACACTACA
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tu C, Xue AJ,
Drmanac RT;
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Wehrman T, Xu
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Wang Z, //
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in gene therapy. A composition containing a polypeptide or polynuclectide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as hizheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression. Activin/inhibin activity, chemotactic/chemokinetic activity, haemotactic/chemokinetic activity, haemotactic/chemokinetic activity, haemotactic/chemokinetic activity, arbhritis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders.
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Zhang J
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Yang Y,
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Drmanac RT;
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Wang Z, Wehrman T, X
Zhou P, Goodrich R,
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25-APR-2000, 2000US-0552117.
9-JUL-2000, 2000US-059042.
19-JUL-2000, 2000US-065312.
03-AUG-2000, 2000US-0655450.
14-SBP-2000, 2000US-065191.
19-OCT-2000; 2000US-063191.
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          immunosuppressant and cytostatic activity. The polymuclectides are useful in gene therapy. A composition containing a polymerlectide or polymuclectide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral scleosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as Immune system suppression, Activin'inhibin activity, chemotactic/chemokinetic activity, haemostatic assays for receptor activity, arthritis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and CNS disorders.
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 polypeptides (AAM38642-AAM42213) with nootropic
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                                                                                                                                                                                                                                                                      Pred. No. 6e-224;
0; Mismatches
                                                                                                                                                                                                                                                          93.8%; Score 1032.4;
99.8%; Pred. No. 6e-22
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Matches 1044; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human, rat, mouse, skin cell; skin wound; cancer, growth defect;
developmental defect; inflammatory disease; dermatological; vulnerary;
immunomodulator; anti-inflammatory; cytostatic; neuroprotective; gene;
839 CATGAAGATCGGCATCGAGGCCAAGAACTTGGCGAGGTACGAGGTCTGCAGCATCCTCCT
                                                                                                                                                                                                       779 GGCCACCTCGACGTGCTGGTGTGGGTGGCGTGATCCGCTACCTGACCTTCTTCCACAA
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TGGCTGTCATCTACCTGGGCTACTGCTTCTGTGGCTTGGATCGTGCTGGGGCCCCTATCATG 1080
               1187 TGGCTGTCATCTACCTGGGCTATTGCTTCTGTGGCTTGGATCGTTCTAGGGCCCCTACCATG 1246
                                                                                                                                                                                                                                                         Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                               DNA encoding novel human diagnostic protein #8078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID No 8078; 103pp; English
                                                                             1267
                                                  TGAAGTTCCGCTCACTCTCCA 1101
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2000US-0649167.
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P-PSDB; ABG08087.
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23-AUG-2000;
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           Length 1827
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           24;
         Score 851.4; DB 24;
Pred. No. 5.5e-183;
0; Mismatches 156;
                                                             CATTCCGGGAAGAGAACACCATCGCCTTCCGACACCTCTT
        77.3%;
85.8%;
                                Matches 945; Conservative
        Query Match
Best Local Similarity
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (FGR) primers, alignmers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags. (Cridentifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical inaging of sites expressing (II). (I) and (II) are useful in medical disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in chapmostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biddiversity printed from WIPO and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.
Note: The sequence data for this patent did not appear in the printer Note: The sequence data for this patent did not appear in the printer ttp.wipo.int/pub/published_pct_sequences. Sequence 2092 BP; 386 A; 668 C; 605 G; 433 T; 0 other;

Score 642.2; DB 23; Length 2092; Pred. No. 1.2e-135;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to novel genes (ABL89449-ABL90853) and proteins (ABB89040-ABB90444) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, or urogenical, (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diseasé, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial isothaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel 1405 isolated polypeptides, useful for diagnosis, treatment and prevention of neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 4; SEQ ID NO 261; 2081pp + Sequence Listing; English.
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                                                                                                                                                                                                                                     Human polynucleotide SEQ ID NO 261.
                                                                                                          ABL89699 standard; cDNA; 734 BP.
    1475 AACTACAATTTCCGC 1489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HUMA-) HUMAN GENOME SCI INC
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                                                                                                                                                                                         (first entry)
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The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polypeptide (II) sequences. (I) is useful as hybridisation probes, composition (ER) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The chromosome composition of (II) is useful in gene therapy techniques (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as companied supplement. (II) and its binding partners are useful in medical inaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations cresponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and adal sequences. Alsofelysty-Alsofesch represent novel human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                 New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
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                                                                                                                                                                                    Claim 1; SEQ ID No 8077; 103pp; English
            Tang YT;
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Matches 461; Conservative
                                              WPI; 2001-639362/73.
P-PSDB; ABG08086.
            Liu C,
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food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA encoding novel human diagnostic protein #8077.
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23-AUG-2000; 2000US-0649167.
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Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                           DNA encoding novel human diagnostic protein #25122.
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                                                                            AAS89318 standard; cDNA; 635 BP.
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Best Local Similarity 100.
Matches 334; Conservative
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RESULT 14
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The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnosfics, forensics, gene mapping, identification of mutations cresponsible for genetic disorders or traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA encoding novel human diagnostic protein #1735.
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                                                                                                                                                                                                                                                                                    335 GGGCCTATCATGTGAGTTCCGCTCACTCTCCA 302
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23-AUG-2000; 2000US-0649167.
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828 GGCACCATCATGAAGATCGGCATCGAGGCCAAGAACTTGGCGAGCTACGACGTCTGCAGC

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CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
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| 308 | at ftp.wipo.int/pub/published_pct_sequences. | |
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| SO | Sequence 776 BP; 141 A; 243 C; 248 G; 144 T; 0 other; | |
| Q A B | Query Match Best Local Similarity 99.0%; Pred. No. 1.9e-54; Matches 295; Conservative 0; Mismatches 2; Indels 1; Gaps 1; | |
| οy | 1 CATTCCGGGAAGAGAACACCATCGCCTTCCGACACCTCTTCTTGGGCTACTCGGACG 60 | |
| Db | 401 CATTCCGGGAAGAGACACCTTCCGACCTCTTCCTGCTGGGCTACTCGGACG 460 | |
| λŏ | 61 GAGCGGATGACACCTTCGCAGCGGGAGCAGCTGTACCAGGCCATCTTCCATG 120 | |
| qq | 461 GAGCGGATGACACCTTCGCAGCCTGCGGGGGGGGCGTGTACCAGGCCATCTTCCATG 520 | |
| ò | 121 CTGTGGACCAGTACCTGGCGTTGCCTGACGTGTCACTGGGCCGGTATGCGTATGTCCCGTG 180 | |
| Dp | 521 CTGTGGACCAGTACCTGGCGTTGCCTGACGTCTCACTGGGCCGGTATGCGTATGTCCGTG 580 | |
| \$ | 181 GTGGGGGTGACCCTTGGACAATGGCTCAGGGGTTGCTCTGCGCAGCGGTACTACCACC 240 | |
| QQ | 581 GTGGGGGTGACCCTTGGACCAATGGCTCAGGGCTTGTTCTCTGCCAGGGGACTACCACC | |
| ò | 241 GAGGCCACGTGGACCGGCCAACGACATTTGACTTGAT-CCGATGGTGGTTACTG 297 | |
| aga | 641 GAGGCCACGGGGCAACGACATTTGACATTGATCCCGATGGTGGTTGTTG 698 | |
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Search completed: October 27, 2003, 12:34:25 Job time : 368.835 secs

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October 27, 2003, 11:10:42 ; Search time 4411.07 Seconds (without alignments) 10211.014 Million cell updates/sec
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| ARIES | Description | AX280021 | AF249319 Homo sap | AK026102 Homo sa | 3 AF287269 Homo sap | BC005149 Homo sap | AX280019 Sequence | 70 - AJ293970 Homo sa | 3 AX083508 Sequence | 59 AJ293659 Homo | 39 AF302009 Mus mus | 51 BC005651 Mus mus | 31 AY083531 Mus mus | 35 AF4/3000 MU | BD156806 Primer f | 3 AK001868 Homo sap | 32 AY083532 Mus mus | 47 BC029847 Mus mus | 75 AF503575 Mus mus | AY083533 Homo sap | SCO44140 Danio re | AFZ8/2/0 HOMO | ACOOSSAS Homo sage | 2S6 AF305577 Homo sap | 2S3 AF305574 Homo sap | 0 AC126740 Rattus n | AC120898 Rat | ACO / 9544 | ANO33348 NO. | 284 AF305575 Hon | 2SS AF305576 Hon | 0 AK094010 Hon | 8 AK095148 Hon | 9 AC017729 Dro | 2 AC009382 Drc | 8 AC069458 Dro | 6 AE003516 Drc | 2 AF482952 Cae | 8 BX284638 Dar | 0 BX511120 Dar | 8 BX537268 Dar | 1 AC013291 Hon |
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| SUMMARIE | А | | 3.5 | 110 | 26 | 14 | 100 | 33 | 50 | HSA2936 | AF3020 | BC0056 | 335 | AF4 / UU | 083 | 86 | AY0835 | 98 | AF5035 | 53 | 1.14 | 7 5 | 2 1 2 | 557 | 557 | 574 | 89 | 954 | 4000 | 57 | 0557 | 9401 | 514 | N | 938 | 945 | 00351 | 295 | 28463 | 51112 | 3726 | 01329 |
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| PAT 02-NOV-2001 | ; Euteleostomi; | |
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| linear | . Vertebrata ii; Hominidae | -2 (tlcc-2) |
| DNA | raniata; starrhin | I. protein- 001; |
| AX280021 Sequence 3 from Patent W00177331 AX280021 AX280021 GI:16607475 | Homo sapiens (human) Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. | 1 Curtis, R.A. and Silos-Santiago, I. Human trp-like calcium channel protein-2 (tlcc-2) Patent: WO 0177331-A 3 18-OCT-2001; |
| RESULT 1 AX280021 LOCUS DEFINITION ACCESSION VERSTON | KEYWORDS SOURCE ORGANISM | REFERENCE AUTHORS TITLE JOURNAL |

ALIGNMENTS

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/db_xref="GI:9971788"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AF249319 2004 bp mRNA linear PRI 22-SEP-2000 Homo sapiens mucolipidosis type IV protein (MLIV) mRNA, complete
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Frumkin,A., Raas-Rothschild,A., Glusman,G., Lancet,D. and Bach,G.
Direct Submission
Submitted (26-MAR-2000) Molecular Genetics, The Weizmann Institute
of Science, P. O. Box 26, Rehovot 76100, Israel
Location/Qualifiers
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(Dases 1 to 2004)

Bargal,R., Avidan,N., Ben-Asher,E., Olender,Z., Zeigler,M.,

Frumkin,A., Raas-Rothschild,A., Glusman,G., Lancet,D. and Bach,G.

Identification of the gene causing mucolipidosis type IV

Nat. Genet. 26 (1), 118-123 (2000)
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                          CCTTCCTCCTCGCCCGCTCACTCCTTCGAGGCTTCCTGCTGCAGAACGAGTTTGTGG
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/organism="Homo sapiens'
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1. .2004
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/gene="MLIV"
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TQAHIQBCKHPSVPGHGDNSFRLLFDVVVILTCSLSFLLCARSLLRGFLLQNEFVGFM
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Conservative 0; Mismatches 0;
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/mol_type="genomic_DN%"
/db_xref="taxon:9606"
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/note="unnamed protein product"
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PRI 29-SEP-2000

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Sugano, S., Suzuki, Y., Ota, T., Obayashi, M., Nishi, T., Isogai, T., Shibahara, T., Tanaka, T. and Nakamura, Y.

Direct Submission
Submitted (29-AUG-2000) Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure Analysis, Human Genome Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:cdnal@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
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LLKYFPMSPCDKFRAKGRKPCKLMLQVVKILVVTVQLILFGLSNQLAVFREENTIAFR
HLFLLGYSDGADDTPAAYTREQLYQA FHAVUQYLALPDVSLGRYAVVRGGGDPWTNG
SGTALCQRYYHRGHVDPANDTFDIDPWVVTDCIQVDPPERPPPERDDLTLLSSSSSSY
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Okamoto,S., Okitani,R., Ota,T., Suzuki,Y., Obayashi,M., Nishi,T.,
Shibahara,T., Tanaka,T., Nakamura,Y., Isogai,T. and Sugano,S.
NEDO human cDNA sequencing project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fax:81-3-5449-5416)
NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5' - & 3' - end one pass sequencing: Departent of Virology and Human Genome Center, Institute of Medical Science, University of Tokyo (partly supported by Science and Technology
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<u> AGATCGGCATCGAGGCCAAGAACTTGGCGAGCTACGACGTCTGCAGCATCCTCCTGGGCA</u>
                   CCTCGACGCTGCTGGTGGGTGGCGTGATCCGCTACCTGACCTTCTTCCACAACTACA
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Homo sapiens
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TQAHTQEKTHBSVPQHONSPRLLFDVVVTLTCSLSFLCARSLLGRGFLQNBEVGFN
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HVKFRSLSWYGECLESLINGDDMFVTFRAMADQQQRSSLVMLFSQLYINSFISLFIN
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SGLALCQRYYRGHVDPANDTPDIDPMVYDCIQUOPPERPPPPPSPDLILLESSSY
KNLTLKFHKLVNVYTHFRLKTILDPMVYDTIFFDVYTFSVLITFDNKAHSGRIPISLE
TQAHIQBCKHPSVYGHGDNSPRLLEDVYVILTCSLSFLLCARSLLRGFLLQNBFVGFM
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HVKFRBLSMYSECLFSLINGDDMFVTFAAMQAQQGRSSLVWLFSQLYLYSFISLFIYM
VLSLFIALITGAYDTIKHPGGAGAEESELQAYIAQCQDSPTSGKFRRGSGSACSLLCC
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Slaugenhaupt, S.A.
Slaugenhaupt, S.A.
Slaugenhaupt, S.A.
Submission
Submitted (13-UUL-2000) Molecular Neurogenetics, Harvard Institute of Human Genetics, 77 Ave. Louis Pasteur, HIM Building Room 422,
Boston, MA 02115, USA
1. .2051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Eukaryota, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 2051)
Sun,M., Goldin,E., Stahl,S., Falardeau,J.L., Kennedy,J.C.,
Acierno,J.S. Jr., Bove,C., Kaneski,C.R., Møgle,J., Bromley,M.C.,
Colman,M., Schiffmann,R. and Slaugenhaupt,S.A.
Mucolipidosis type IV is caused by mutations in a gene encoding a novel transient receptor potential channel
Hum. Mol. Genet. 9 (17), 2471-2478 (2000)
                                                                                                                                                                                                         TGGCTGTCATCTACCTGGGCTACTGCTTCTGTGGCTTGGATCGTGCTGGGGCCCCTATCATG
                                1270 CCTCGACGCTGCTGGTGTGGGGGGGGGAATCCGCTACCTGACCTTCTTCCACAACTACA
                                                                                                                                                                                  TGGCTGTCATCTACCTGGGCTACTGCTTCTGTGGCTGGATCGTGGGGCCCCTATCATG
                                                                                           ATATICCTCATCGCCACACACTGCGGGTGGCCCTGCCCAGCGTCATGCGCTTCTGCTGCCG
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/product="mucolipin"
/protein_id="AAG00797.1"
/db_xref="G1:9844924"
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/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="19"
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1. .2051
/gene="MCOLN1"
126. .1868
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TQAHIOECKHPSVFQHGDNSFRLLFDVVVILTCSLSFLLCARSLLRGFLLQNEFVGFM
WRQRGRVISLWERLEFVNGWYILLVTSDVLTISGTIMKIGIEAKNLASYDVCSILLGT
STLLVWVGVIRYLFFFHNYNILIATLRVALPSVWRFCCCVAVIYLGYCPCGWIVLGPY
HVYFRSLSMVSECLFSLINGDDMFVTFAAMQAQQGRSSLVWLFSQLXSFISLFIXW
VLSLFTALITGAYDTIKHPGGAGAEESELQAYIAQCQDSPTSGRFRRGSGSACSLLCC
CGRDPSEEHSLLVN"
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Best Local Similarity 100.0%; Pred. No. 9.6e-195;
Matches 1101; Conservative 0; Mismatches 0; Indels 0;
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HVKRRSLSMYSECLFSLINGDDMFVTFAAMQAQQGRSSLVWLFSQLYLYSFISLFIYM
VLSLPIALITGAYDTIKHPGGAGAEESELQAYIAQCQDSPTSGKFRRGSGSACSLLCC
1420 IGGCIGICAICIACCIGGGCIACIGCIICIGIGGCIGGAICGIGCIGGGGCCCIAICAIG 1479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia
Greene, Mark Ketteman and Anuradha Madan
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2087)
Strausberg,R.
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                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens, mucolipin 1, clone MGC:3287 IMAGE:3507836, mRNA.
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/tissue_type="Brain, neuroblastoma"
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Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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Human trp-like calcium channel procein-2 (tlcc-2)
Patent: Wo 0177331-A 1 18-OCT-2001;
MILLENIUM PHARMACEUTICALS, INC. (US)
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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  2037 bp mRNA lin
Homo sapiens mRNA for mucolipidin (ML4 gene).
AJ293970
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ML4 gene; mucolipidin.
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Homo sapiens
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/produce="mucolipidin"
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(5), 1110-1120 (2000)
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81.1823
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                                                                                               Borsani, G.
Direct Submission
Submitted (08-SEP-2000) Borsani
Milano, ITALY
                                                                                                                                                                                                                                                                  /mol_type="mRNA"
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1. .2037
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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/ PERCENT_id="CACO7813.1"
/ PERCENT_id="CACO7813.1"
/ Che xref="GI:1004513"
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VLGSGHVAGDAGTWGRRGPEDAPDPHPSLLPRLVNVTTHFRLETVNGSTLLUVTGSL
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SFLLCARSLLRGFLLQNEFVGFWWRQRGRVISLWFRLEFVNGWYILLVTSDVLITGSL
INK.GIEBAXNLASYDVCSILLGTSTLLWWGVIRYLFPFHNYNILIATLENVALDSGVWR
PCCCVAVIYLYFFFRANSFOLDENTSTLLWWGVIRYLFFPHNYNILIATLENVALDSGVWR
PCCCVAVIYLYFFFRANGSSCSLCCCGRDPSBEHSLLVN"

CQDSPTGRFRRGSGSSACSLLCCCGRDPSBEHSLLVN"

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                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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alternative splicing; ML4 gene; mucolipidin.
Homo sapiens (human)
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Pred. No. 6.6e-149;
0; Mismatches 1;
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Submitted (O2-AUG-2000) Borsani G.,
and Medicine - TIGEM, Via Olgettina
Revised by author
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Homo sapiens mRNA for mucolipidin,
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/db_xref="taxon:9606"
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LLKYFPNSPCDKTRAKGRKPCKLMLOVVKILVVTVQLILFGLSNQLVVTFREENTIAFR
LLKYFPNSPCDSPDTFAATTOGOLYGAPTPANDOVILIPPEIGNSAVYOTGGGGSPANG
SALALOGRYYHRGHVDFANDTPDIDFRYVTDCIQVDFPDRPPDIPSEDLDFLDGSASY
KNLTLKFHKLINVTIHPQLKTINLQSLINNEIPDCYTFSILITFDNKAHSGRIPIRLE
TXTHIQECKTRSCYSRHGDNSFRLLFDVVVILTCSLSFLLCARSLLRGFLLQNEFVFM
WRRGREISLWBLEFWNGWYILLYTSUVLTISGTVMKTGISTAKNLASYDVGSILLGT
STLLVWWGVYIYLTATLSTRAYBLBSWRFCCCVAVIYLGYCFCGWIVLGFY
HVKFRSLSMVSBCLFSLINGDDMFVTFAAMQAQQGHSSLVWLFSQLYLYSFIGHFTW
VLSLFIALITGAYDTIKHPGGTGTEKSELQAYIEQCDSSTTGKFRRGSGSACSLFCC
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Location/Qualifiers
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Cloning and characterization of the mouse Mcolni gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAGCGGATGACACCTTCGCAGCCTACACGCGGGAGCAGCTGTACCAGGCCATCTTCCATG 120
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CTCATCGCCACACTGCGGGTGGCCCTGCCCAGCGTCATGCGCTTCTGCTGCTGCGTGGCT
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Falardeau, J.L., Kennedy, J.C., Acierno, J.S., Sun, M., Stahl, S. Goldin, B. and Slaugenhaupt, S.A.
Direct Submission
Submitted (30-AUG-2000) Molecular Neurogenetics, Harvard Ins of Human Genetics, 77 Ave. Louis Pasteur, Boston. MA 02115.
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Mus musculus mucolipin-1 (Mcoln1) mRNA, complete cds.
AF302009
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1. .2003
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85.8%; Pred. No. 2.4e-148;
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'protein_id="AAL58667.1"
'db_xref="GI:18086904"
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/db_xref="taxon:10090"
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76. .1818
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KEYWORDS
SOURCE
ORGANISM
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LOCUS
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ACCESSION VERSION KEYWORDS SOURCE

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AUTHORS

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LKYPFRSPCTKFRAKGRKPCKLMLQVVKILVVTVQLILFGLSNQLVVTFREENTIAFR
HLFLLGYSDGSDDFRAAYTOBQLYQAIFYAVDGYLILPEISLGKYAYVRGGGGPWANG
SALALCQRYWRGHVDPANDTFDIDFRVYDCIQVDPDRPPDIPSEDLDFLDGSASY
KNLTLKFHKLINVTHPGLKTINLOGLINNETPDCYYFSILITFDNKAHSGRIPTRE
TKTHIQECKHPSVSRHGDNSFRLLFDVVVILLTCSLSFLLCARSLLRGFLLQNEFVVFM
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VLSLFIALITGAYDTIKHPGGTGTEKSELQAYIEQCQDSPTSGKFRRGSGSACSLFCC
CGRDSPEDHSLLVN"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           533 GIGGGGGGGCCTIGGGCCAAIGGAICAGCITIGGCICICIGCCAGCGGIACIACCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 GAGGCCACGTGGACCCGGCCAACGACATTTGACATTGATCCGATGGTGGTTACTGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGGATGGCAGGGCCAGTTACAAGAACCTCACACAGAAATTCCACAAGCTGATCAACGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ccarccacriccagcrigaadacaarraaccriccagdaccricarcaacaargagarccrig
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTGTTACACCTTCAGTATCCTGATCACATTTGACAATAAAGCGCACAGTGGGCGAATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          893 ccarcceccredagaccaaagacccacarccagagrecaaacaccccagrercccagac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CATTCCGGGAAGAGACACCATCGCCTTCCGACACCTCTTCCTGCTGGGCTACTCGGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGGAAAGCAGCTCCAGTTACAAGAACCTCACGCTCAAATTCCACAAGCTGGTCAATGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      541 CCATCAGCCTGGAGCCCAGGCCCACATCCAGGAGTGTAAGCACCCCAGTGTCTTCCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 10; Length 2039;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 851.4; DB 10;
Pred. No. 2.4e-148;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          533 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 85.8%;
Matches 945; Conservative
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                                                                                .. .2039
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               be found
                            BC005651 2039 bp mRNA linear ROD 16-APR-2003
Mus musculus mucolipin 1, mRNA (cDNA clone MGC:7172 IMAGE:3257440),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ä
                                                                                                                                                                                          Mus musculus (house mouse)
Mus musculus
Busaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae; Mus
1 (bases 1 to 2039)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 6 Row: c Column: 16 This clone aselected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (02-APR-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: anm@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIH-MGC Project URL: http://mgc.nci.nih.gov

    .2039
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                                                                                                                                               BC005651.1 GI:13542918
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                                                                                        complete cds.
BC005651
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                                  LOCUS
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AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PUBMED
                                                                                                                                                                                                                                                                                                            REFERENCE
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REMARK COMMENT

TITLE

FEATURES

Gaps

42;

9

180 385

120

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493

709 540 769 599 829 654 889 714 774

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTTTCAAAGAGGAGAACACTATAGCCTTCAAACACCTCTTCCTAAAGGGCTACATGGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             326 GAATGGACGACACTATGCAGTGTACACTCAGAGTGAAGTGTATGACCAGATCATCTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTGTGGACCAGTACCTGGCGTTGCCTGACGTGTCACTGGGCCGGTATGCGTATGTCCGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GIGGGGGGGCTTGCCAATGCCTCAGGGCTTGCTCTCTGCCAGCGGTACTACCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAGGCCACGTGGACCCGGCCAACGACACATTTGACATTGATCGATGGTGGTTACTGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     650 AGCTCCAGTTTAAGCTCAAAGCCATCAATCTGCAGACAGTTCGACACCAGGAGCTTCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACTIGCTATACCTTCAGCGTCCTGATCACGTTTGACAACAAAGCACACAGTGGGCGGATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTGTGGGGGTTCATGTGGCGGCAGCGGGACGGGTCATCAGCCTGTGGGAGCGGCTGGAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                    CATTCCGGGAAGAGACACCATCGCCTTCCGACACCTCTTCCTGCTGGGCTACTCGGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 GAGCGGATGACACCTTCGCAGCCTACACGCGGGAGCAGCTGTACCAGGCCATCTTCCATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                494 AAGGAACCATCTGCCCCGGGAACGACACCTTTGACATCGATCCAGAAGTTGAAACAGAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCATCCAGGTGGATCCCCCCGAGCGGCCCCCTCCGCCCCCCAGCGACGATCTCACCCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTTTCCTTGTAGAGCCAGATGAAGCTTCCCACCTTGGAACCCCTGGAGAAATAAACTC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGGAAAGCAGCTCCAGTTACAAGAACCTCAAGCTCAAATTCCACAAGCTGGTCAATGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    421 CCATCCACTTCCGGCTGAAGACCATTAACCTTCCAGAGCCTCATCAATAATGAGATCCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <u> actigitraceactitracericactatraceritecaciacaacecteacacaciceaacaatea</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                541 CCATCAGCCTGGAGACCCCAGGCCCACATCCAGGAGTGTAAGCACCCCCAGTGTCTTCCAG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     aaataagcrtaagacaactarcraticaaagaaticcaaagactggcatgrictggat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----CACGGAGACAACAGCTTCCGGCTCCTGTTTGACGTGGTGGTCATCCTCACCTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        830 CAATTCAGAAGAACACACACTACATGATGATCTTTGATGCCTTTGTCATTCTGACCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCCTGTCCTTCCTCCTCTGCGCCCGCTCACTTCGAGGCTTCCTGCTGCAGAACGAGT
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                                                                                                                                                                                                                                                                                                                                                   DB 10; Length 1662;
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                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                               Score 317.8; DB 10;
Pred. No. 3.8e-49;
0; Mismatches 422;
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                                                                                                                                                                                                                                                                                   383 g
                                                                                                                                                                                                                                                                                                                                                 28.9%;
                                                                                                                                                                                                                                                                                      405 C
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Di Palma, F. and Noben-Trauth, K.

Direct Submission

Direct Submission

Submitted (11-MAR-2002) National Institute on Deafness and Other

Communication Disorders, National Institutes of Health, 5 Research

Court, Rockville, MD 20850, USA

Location/Qualifiers
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Mus musculus
Eukaryora; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryora; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1662)
Di Palna, F., Belyantseva, I.A., Kim, H.J., Vogt, T.F., Kachar, B. and
Noben-Trauth, K.
Mutations in Mcoin3 associated with deafness and pigmentation
defects in varitint-waddler (Va) mice
Proc. Natl. Acad. Sci. U.S.A. 99 (23), 14994-14999 (2002)
ATGGAGACAACAGCTTCCGGCTTCTGTTTGATGTGGTGGTTATCCTCACCTGCTCCTGT
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      Length 1712;
                                                                  Indels
      DB 10;
Score 317.8; DB 10;
Pred. No. 3.8e-49;
0; Mismatches 422;
      28.9%;
58.1%;
      Query Match 28.9
Best Local Similarity 58.1
Matches 643; Conservative
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SIQKNTHYMMIFDAFVILTCLASLVLCARSVIRGLQLQQEFVNFFLLHYKKEVSASDQ
MEFINGWYINIIISDILTIVGASVLKMETQAKSHTSYDVGSILGGTSKHJWLGYTRYL
GFFAKYNLLIILLQAALDYWRFCCCAAMIYLGYCFCGMIVLGPYHERFRSLNRVSEC
LRSLINGDDMFGFFARMQQKSYLWHERRYYLYSFISLBTYMILSLFTALITDTYFTI
KHYQQDGFPFTELRKFIAECKDLPNSGKYRLEDDPPGSLLCCCKK"
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LKGYMDRMDDTYAVYTQSEVYDQIIFAVTQYLQLQNISVGNHAYENKGTKQSAMAICQ
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Falardeau, J.L., Kennedy, J.C., Acierno, J.S. and Slaugenhaupt, S.A. Cloning of the mouse Mcoln3 gene
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Falardeau, J.L., Kennedy, J.C., Acierno, J.S. and Slaugenhaupt, S.A. Direct Submission
Submitted (24-JAN-2002) Molecular Neurogenetics, Harvard Institu of Human Genetics, 77 Ave. Louis Pasteur, HIM Building Room 422, Boston, MA 02115, USA
      1010 TCATCAACGGGTGGTACATTATGATCATTAGTGACATATTGACAATCGTTGGATCAG
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Mus musculus mucolipin-3 (Mcoln3)
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/mol_type="mRNA"
/strain="C57BL6/J"
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BD156806 17-JAN-2003
Primer for synthesizing full-length cDNA and use thereof.
BD156806.1 GI:27862564
JP 2002191363-A/11649.
Homo sapiens (human)
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            ----GAGAACAAAGGTACCAATCTGCTATGGCAATCTGTCAGCACTTCTACAAGC
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                                                                                                                                                                                                                                                                                                                                                  361 TGGAAAGCAGCTCCAGTTACAAGAACCTCACGCTCAAATTCCACAAGCTGGTCAATGTCA
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HFYKRGNIYPGNDTPAVTOSDYDOLIFARMOYDLOLIVNSVGWRHAYBRKCFRORGSAMAICO

HFYKRGNIYPGNDTPELFETECFPVEPDBFFHIGTPABNKLNITLDFHRLITTVE

OFKLKAINLGTVRHQELPDCYDFTLITIFDNKAHSGRIKISLDNDISIREKCKDWHVSG

SIQXYHTYMMMFDAFVILTCYNSLILCIRSVIRGOLOLOGOFFWFFLLHYKKEVSVSDO

MEFVNGWYIMIISONILTHIGSILKMEIQAKSLTSVDVCSILLGTSTMLVWLGVIRYI

GFFAKYNLLILTLQAALDNVIRFCCCAAMIYLGYGCGGWIVLGPYHDKFKSLMWVSE

LRSLINGDDWFATFARWQKSYLVWLFSRIYTYSFIGLFIYMILSLFIALITDTYSTI

SQCOOGFFFFFRENCHENGCKYRLEDDFPVSLFCCKK"

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03-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
2 (bases 1 to 1900)
2 (bases 1 to 1900)
2 (bases 1 to 1900)
Direct Submission
Submitted (24-JAN-2002) Molecular Neurogenetics, Harvard Institut of Human Genetics, 77 Ave. Louis Pasteur, HIM Building Room 422, Boston, MA 02115, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Slaugenhaupt, S.A.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 1900)
Falardeau, J.L., Kennedy, J.C., Acierno, J.S. and Slaugenhaup
Cloning of the MCOLN3 gene
                                                                                                                                                                                                                                                                                                               PRI
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                                                                                                                                                                                                                                                                                            AF475085 1900 bp mRNA linear F
Homo sapiens mucolipin-3 (MCOLN3) mRNA, complete cds.
AF475085
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Pred: No. 1.4e-45;
0; Mismatches 434; Indels
                                                                                                                                   ACCATGAGAGTTCCGTTCCCTGAACA 1338
                                                                                                    ATCATGTGAAGTTCCGCTCACTCTCCA 1101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="mucolipin-3"
/protein_id="AAL84622.1"
/db_xref="G1:19072754"
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/chromosome="1"
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631; Conservative C
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completed: October 27, 2003, 15:41:57
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                         C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N1S/00,C12N5/00
ner for synthesizing full-length cDNA and use thereof FH K
Location/Qualifiers
CDS (54). (1544).
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23.7%; Score 260.8; DB 6; Length
Best Local Similarity 57.6%; Pred. No. 1.5e-38;
Matches 525; Conservative 0; Mismatches 357; Indels
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                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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910 ACATTATGATTATTATTAGTGACATATTGACAATCATTGGATCAATTCTAAAAATGGAAA
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                                                                                          790 ACAICCIGCICGICACCAGCGAIGIGCICACCAICICGGGCACCAICAIGAAGAIGGGCA
                                                                                                                                                                                                                                                                      850 TCGAGGCCAAGAACTTGGCGAGCTACGACGTCTGCAGCATCCTCCTGGGCACCTCGACGC
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Sequence 50, Appl
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Sequence 608, Appl
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Sequence 161, App
Sequence 28893, A
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Seguence 21, App
                                                                                                                                          October 27, 2003, 12:19:17; Search time 63.6775 Seconds (without alignments) 8465.189 Million cell updates/sec
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Sequence 4, Ap
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/ Cgn2_6/ptodata/1/pubpna/PCT_NBW_PUB.seq:*
/ Cgn2_6/ptodata/1/pubpna/PCT_NBW_PUB.seq:*
/ Cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
/ Cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
/ Cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
/ Cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
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/ Cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-866-050A-608
US-10-152-661-608
US-09-918-995-27041
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US-09-864-761-28893
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US-09-965-529-50
US-09-969-680A-50
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US-10-305-810-4
US-10-114-153-21
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Maximum Match 100%
Listing first 45 summaries
                                                                                                OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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| 7 Sequence 107 | Sequence 107 | 7 Seguence 107 | Sequence 107 | Sequence 107 | Sequence 107 | 107 Sequence 107, App | 83 Seguence 183 | 02 Sequence 802 | 3 Sequence 23, | 7 Seguence 27, | 5 Seguence 25, | 0 Seguence 10, | 10, | 0 Seguence 10, | 0 Seguence 10, | equence 10, | 0 Seguence 10, | 816 Seguence 581 | -1 Sequence 1, App | Sequence 3, | 4 Seguence 14, | Seguence 14, | Seguence 1, | Sequence 283 | 83 Sequence 283 | 159 Sequence 51 | 27 Seguence 42 | Sequence 22, |
|----------------|--------------|----------------|--------------|--------------|--------------|-----------------------|-----------------|-----------------|----------------|----------------|----------------|----------------|----------------|----------------|----------------|----------------|----------------|------------------|--------------------|----------------|----------------|----------------|----------------|----------------|-----------------|-----------------|----------------|----------------|
| US-09-992 | US-09-924-34 | US-09-992 | US-10-154 | 08-09-99 | US-10-000 | -10-000-986- | US-09-746-783- | US-10-037-270- | US-10-114-153- | US-10-114-153- | US-10-114-153- | US-10-140-472- | US-10-141-761- | US-10-142-885- | US-10-158-790- | US-10-123-155- | US-10-146-731- | US-10-156-761- | 4 US-10-156-761 | US-10-294-804- | US-10-291-230- | US-10-291-249- | US-10-278-751- | US-10-050-898- | US-10-050-902- | US-10-156-761- | US-10-037-270- | US-09-953-348- |
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ALIGNMENTS

RESULT 1
US-09-828-466-3
US-09-828-466-3
Sequence 3, Application US/09828466
Fatent No. US20020035056A1
GENERAL INFORMATION:
APPLICANT: Curtis, Rory A.J.
APPLICANT: Silos-Santiago, Immaculada
TITLE OF INVENTION: 54420, A NOVEL HUMAN CALCIUM CHANNEL
FILE REFERENCE: MNI-125CP
CURRENT APPLICATION NUMBER: US/09/828,466
CURRENT APPLICATION NUMBER: US 09/544,797
FRIOR PAILING DATE: 2001-04-06
FRIOR APPLICATION NUMBER: US 09/544,797
NUMBER OF EQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 1740
TYPE: DNA
FRATURE:
FRATURE:
NAME/KEY: CDS
JUCATION: (1)...(1740)
US-09-828-466-3

Query Match
Best Local Similarity 99.3%; Pred. No. 1.1e-32;
Matches 143; Conservative 0; Mismatches 1; Indels 0; Gaps

Matches 143; Conservative 0; Mismatches 1; Indels 0; Gaps

Qy 1356 GAGTTCGGCTCATGGTGTCTGAGTGCTGTTCTCGCTCATCAATGGGGACGA

Qy 118 CATGTTGTGACGTTCGCCCCATGCTGTTCTCGCTCATCAATGGGGACGA

Qy 118 CATGTTTGTGACGTTCGCCCCATGCAGGCCCAGCAGCAGCCTGGTGTGTCACGCT

1415

111

177

0

1475

178 CTTCTCCCAGCTCTACCTTTACTC 201

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Score 142.4; DB 10
Pred. No. 1.1e-32;
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                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 50, Application US/09969680A; Publication No. US20030124649A1; GENERAL INFORMATION:
      70.8%;
Query Match
Best Local Similarity 99.3
Matches 143; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                US-09-969-680A-50
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APPLICANT: TANG, Y. Tom
APPLICANT: TANG, Y. Tom
APPLICANT: BANDMAM, Olga
APPLICANT: BANDMAM, Olga
APPLICANT: BANGRAM, Alada
APPLICANT: AZIMZAI, Yalda
APPLICANT: BANGRAM, Mariah R.
APPLICANT: LU, Dyung Aina M.
APPLICANT: DY DYUNG AINA M.
APPLICANT: DY DYUNG AINA M.
APPLICANT: DY DYUNG AINA M.
APPLICANT: DATTERGON, Chandra
TITLE OF INVENTION: MEMBRANE ASSOCIATED PROTEINS
FILE OF TANTENTION NUMBER: US/09/965,529
CURRENT APPLICATION NUMBER: 60/149,641; 60/164,203; PCT/US00/22315
PRIOR PILING DATE: 1999-08-17; 1999-11-09; 2000-08-14
NUMBER OF SEQ ID NOS: 74
SOFTMARE: PERL PROGRAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 13; Length 1740;
                                                                    Sequence 3, Application US/10103458
Publication No. US20020197680A1
GENERAL INFORMATION:
TITLE OF INVENTION:
FILE REPERRICE: MNI-125
CURRENT APPLICATION NUMBER: US/10/103,458
CURRENT APPLICATION NUMBER: US/10/103,458
CURRENT FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: US/09/544,797
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 3
SEQ ID NO 3
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US-09-965-529-50
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Pred. No. 1.1e-
0; Mismatches
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Publication No..US20020182671A1
GENERAL INFORMATION:
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Best Local Similarity 99.3%;
Matches 143; Conservative
                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: LAL, Preeti
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US-10-103-458-3
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NAME/KEY: CDS
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US-09-965-529-50
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LENGTH: 2052
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1463 GAAGTICCGCICACICICAIGGIGICTGAGIGCCIGITCICGCICAICAAIGGGGACGA 1522
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   Length 2052;
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                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030124649A1 977658CB1
US-09-966-80A-50
DB 10;
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APPLICANT: LAL, Freet; YUE, Henry
APPLICANT: LAL, Y. Tom; BANDMAN, Olga
APPLICANT: BURFORD, Neil; AZIMCAI, Yalda
APPLICANT: BURFORD, Neil; AZIMCAI, Yalda
APPLICANT: BAUGHN, Mariah R.; LU, Dyung Aina M.
APPLICANT: PATTERSON, Chandra
ITLE OP INVENTION: MEMBRANE ASSOCIATED PROTEINS
ITLE REPERENCE: PP-0731-1 USA
CURRENT FILING DATE: 200-10-02
FRIOR PLING DATE: 2000-08-14
PRIOR PLING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/149,641
PRIOR APPLICATION NUMBER: 60/149,641
PRIOR PLING DATE: 1999-08-17
PRIOR FILING DATE: 1999-08-17
PRIOR FILING DATE: 1999-08-17
SOFTWARE: PELL PROGRAM
SEQ ID NOS: 74
LENGTH: 2052
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Patent No. US20020076705A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 31 Human Secreted Proteins
FILE REFERENCE: PZ033P1
                                                        0; Mismatches
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1556 CATGITIGIGACGITCGCCGCCATGCAGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGTGTGGCTI 1615
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86.5%; Pred. No. 8.8e-27;
ive 0; Mismatches 21; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 608, Application US/09866050A
Sequence 608, Application US/09866050A
Seneral invormation.
General invormation.
APPLICANT: Watson, James D.
APPLICANT: Stream, Lorna
APPLICANT: Stream, Matthew
APPLICANT: Stream, James G.
APPLICANT: Murison, James G.
APPLICANT: Kumble, Krishanand D.
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: And Methods for Their Use
FILE REFERENCE: 11000.1011c4U
CURRENT FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 725
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                 APPLICANT: Curtis, Rory A.J.
TITLE OF INVENTION: 54420, A NOVEL HUMAN CALCIUM CHANNEL
FILE REFERENCE: MNI-125
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Pred. No. 1.1
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CURRENT FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: US/09/544,797
PRIOR FILING DATE: PRIOF FILING DATE: 200
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin Ver. 2.0
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             1616 CITCICCCAGCICIACCITIACIC 1639
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                                                                                                                                 Sequence 1, Application US/10103458
Publication No. US20020197680A1
GENERAL INFORMATION:
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99.3%;
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Best Local Similarity 86.59
Matches 135; Conservative
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Best Local Similarity 99.3
Matches 143; Conservative
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; LOCATION: (141)..(1880)
US-10-103-458-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens

// TYPE: DNA
// ORGANISM: Mouse
US-09-866-050A-608
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LENGTH: 2095
                                                                                                                 US-10-103-458-1
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Fatent No. US20020035066A1
GENERAL INFORMATION:
APPLICANT: Curtis, Rory A.J.
APPLICANT: Silos-Santiago, Immaculada
FILE OF INVENTION: 54420, A NOVEL HUMAN CALCIUM CHANNEL
FILE REFERENCE: MNI-125CP
CURRENT APPLICATION NUMBER: US/09/828,466
CURRENT FILING DATE: 2001-04-06
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 7
SOFTMARE: Patentin Ver. 2.0
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Pred. No. 1.1e-32;
0; Mismatches 1;
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CURRENT APPLICATION NUMBER: US/09/820,893; CURRENT FILING DATE: 2001-03-30; PRIOR APPLICATION NUMBER: 09/531,119; PRIOR PILING DATE: 2000-32.0; PRIOR PILING DATE: 1908-10-02; PRIOR FILING DATE: 1998-10-02; NUMBER OF SEQ ID NOS: 140; SOFTWARE: Patentin Ver. 2.0; SQQ ID NO 26; LENGTH: 2094
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LOCATION: (2078)
: OTHER INFORMATION: n equals a,t,g, or US-09-820-893-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70.8%;
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Best Local Similarity 99.33
Matches 143; Conservative
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Best Local Similarity 99.3
Matches 143; Conservative
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; LOCATION: (141)..(1880)
US-09-828-466-1
                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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LENGTH: 2095
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60.7%; Pred. No. 0.0046; Mismatches 50; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/10305810
Publication No. US20030176385A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Ju, Jingfang
APPLICANT: Huang, Chunli
APPLICANT: Zhong, Hainbrag
APPLICANT: Simons, Jan Fredrik
APPLICANT: Tailon, Bruce E.
APPLICANT: Chant, John S.
                                                                      91; Conservative
                                 Best Local Similarity
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APPLICANT:
APPLICANT:
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                                                                      Matches
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75.0%; Pred. No. 1.4e-05;
tive 0; Mismatches 21; Indels 0; Gaps
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CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 957
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 676
LENGTH: 668
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OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.5

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.57

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.46

OTHER INFORMATION: SWISSPROT HIT: Q13563, EVALUE 6.00e-03

OTHER INFORMATION: EST HUMAN HIT: M41861.1, EVALUE 5.00e-08

US-09-864-761-28893
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PA125
                                            PRIOR APPLICATION NUMBER: PCT/USU1/0066/
PRIOR PILLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2000-01-30
PRIOR PILING DATE: 2000-01-29
NUMBER OF SEQ ID NOS: 49117
SEQ ID NO 28893
LENGRADIANTER: AND ADDRESSED DESTORMATER: AND ADDRESSED DESTORMATER DESTO
                                 PRIOR APPLICATION NUMBER: PCT/US01/00667
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Publication No. US20030050231A1
GENERAL INFORMATION:
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; ORGANISM: Homo sapiens
US-09-764-872-676
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ORGANISM: Homo sapiens
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Best Local Similarity
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NUMBER OF SEQ ID NOS: 47
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APPLICANT: Chaft. John A.
APPLICANT: Milet. Isabelle
TITLE OF INVENTION: ANTIENSE MODULATION OF PROTEIN EXPRESSION
FILE REPERENCE: 21402-501
CURRENT APPLICATION NUMBER: 06/334,148
PRIOR PILING DATE: 2001-11-29
PRIOR APPLICATION NUMBER: 60/336,572
PRIOR PILING DATE: 2001-12-04
PRIOR APPLICATION NUMBER: 60/192,838
PRIOR PILING DATE: 2000-07-26
PRIOR APPLICATION NUMBER: 60/192,838
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-04-03
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1321 AIGTITGCAACCTITGCCCAAATCCAGCAGAAG-----AGCATCTTGGTGTGGCTG 1371

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Search completed: October 27, 2003, 18:02:14 Job time: 75.6775 secs

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October 27, 2003, 10:28:31 ; Search time 65.3268 Seconds (without alignments) 8305.735 Million cell updates/sec
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Copyright (c) 1993 - 2003 Compugen Ltd.
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| Description | Human immune/haema Human immune/haema DNA encoding novel DNA encoding novel DNA encoding novel Human TLCC-2 proce Human TRP-like cal Human polynucleoti |
|-------------------------------|---|
| SUMMARIES | AAK73827 AAK73826 AAS89322 AAS89310 AAS72274 ABL40755 AAI71700 AAI59236 |
| DB | 00000000000000000000000000000000000000 |
| % Query Match Length DB | 11365 20046 3371 3371 2092 1740 1740 |
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| Score | 1443.4 1443.2 1443.2 1443.2 1423.2 1423.4 |
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| Human membrane ass | polynucleo | Human secreted pro | Human TLCC-2 prote | Human TRP-like cal | DNA encoding novel | Human polynucleoti | Murine cDNA isolat | Human brain expres | m | liver | 0.1 | \sim | | | singl | | rence | digestive s | n NOV9a | librar | n JNK3-bindin | ed protein | Human polynucleoti | Human polynucleoti | Human secreted pro | n | n | V9C | sophila n | hila n | sotide s | ein Barı | ein Barr viru | thering p | tide sequen | Epstein-Barr virus |
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ALIGNMENTS

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17-NOV-2000;
17-NOV-2000;
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Ruben SM; Rosen CA,

WPI; 2001-483426/52

Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -

Disclosure; SEQ ID NO 28639; 3071pp + Sequence Listing; English.

AAKS4951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome

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                         14-AUG-2000;
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23-AUG-2000;
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01-SEP-2000;
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25-SEP-2000; 2
25-SEP-2000; 2
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27-SEP-2000; 2
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29-SEP-2000;
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that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polymucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polymucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic derived cells. AAK64703 to AAK67694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK64922 to AAK54950 and AAM82169 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                              GTTCCGCTCACTCTCCATGGTGTCTGAGTGCCTGTTCTCGCTCATCAATGGGGACGACAT 120
                                                                                                                                                                                                                                                                                                                                                                                         7641 GITCCGCTCACTCTCCATGGTGTCTGAGTGCCTGTTCTCGCTCATCAATGGGGACGACAT
                                                                                                                                                                                                                                                                   Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                                                                                                                                                                        0; Gaps
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                                                                                                                                                                                                       100.0%; Score 201; DB 22; Length 11365; 100.0%; Pred. No. 6.3e-44; cive 0; Mismatches 0; Indels 0;
                                                                                                                                                                        Sequence 11365 BP; 2407 A; 3320 C; 3153 G; 2485 T; 0 other;
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16-MAR-2000; 2000US-018974.
17-MAR-2000; 2000US-0199075.
18-APR-2000; 2000US-0198123.
19-MAY-2000; 2000US-0205515.
07-UNA-2000; 2000US-0205467.
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30-JUN-2000; 2000US-0215135.
07-JUL-2000; 2000US-0216847.
11-JUL-2000; 2000US-0217487.
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2000US-0220964
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Best Local Similarity 100.
Matches 201; Conservative
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amino acid sequences given in MAM82170 to AAM91921. (I) have cytosfettic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, dispansis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to polynucleotides may be used to product the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703 to AAX87694 represent human immune/haematopoietic antigen genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and
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2000US-0251030.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 GIICCGCICACCICCAIGGIGICICAGGIGCCIGIICICGCICATCAAIGGGGACGACAI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 GTTTGTGACGTTCGCCGCCATGCAGGCGCAGGGCCGCAGCAGCAGCAGCTGGTGGCTCTT 180
                                         represent sequences used in the exemplification of the present invention.
sequences from the present invention. AAK54942 to AAK54950 and AAM82169
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                                                                                                                                                                                           100.0%; Score 201; DB 22; Length 20046; 100.0%; Pred. No. 6.9e-44; ive 0; Mismatches 0; Indels 0;
                                                                                                                Seguence 20046 BP; 4133 A; 5821 C; 5659 G; 4433 T; 0 other;
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23-AUG-2000; 2000US-0649167.
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Best Local Similarity
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109 TGGGGACGACATGTTGTGACGTTCGCCGCCATGCAGGCGCAGCAGGGCCGCAGCAGCAGCT 168
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a food supplement, (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequence of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from MIPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 143.4; DB 23; Length 3371; Pred. No. 1e-28;
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                                                                                                                                                                                                                                                                                                                                                                                                  ftp.wipo.int/pub/published_pct_sequences.
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polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (1) is useful in gene therapy techniques to restore normal activity of (11) or to treat disease states involving quantitating a polypeptide in tissue, as molecular weight markers and a food supplement: (11) and its binding partners are useful in medical imaging of sites expressing (11). (11) and its binding partners are useful in medical fusorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations and to produce other trypes of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human
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                                                                                                                                                                                                                                                            diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
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food supplement; medical imaging; diagnostic; genetic disorder; ss.
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 gene mapping, and in recombinant production of (II).
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P-PSDB; ABG08087.
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Note: The sequence and for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO very
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38 CTGACCCCGCCCCCCTCTGGCAGTTCCGCTCACTCTCCATGGTGTCTGAGTCCCTGTTC 97
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                                                                                                                                                       The invention relates to isolated polynucleotide (I) and
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                                                         Claim 1; SEQ ID No 8078; 103pp; English.
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 \begin{array}{c} \mathsf{X} & \mathsf{M} \\ \mathsf{M} \\ \mathsf{X} & \mathsf{M} \\ \mathsf{M} \\ \mathsf{M} \\ \mathsf{M} & \mathsf{M} \\ \mathsf{M} \\ \mathsf{M} \\ \mathsf{M} & \mathsf{M} \\ \mathsf{M} \\ \mathsf{M} \\ \mathsf{M} & \mathsf{M} \\ \mathsf{M} \\ \mathsf{M} & \mathsf{M} \\ \mathsf
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The invention relates to a novel transient receptor potential (TRP)-like calcium channel, designated TLCC-2 and polymolecrides encoding the TLCC-2. TLCC-2 can be expressed by standard recombinant methodology. The TLCC-2 polypeptide, polymolecrides and modulators are useful for treating central nervous system disorders such as neurodegenerative disorders for example Alzheimer's disease, Parkinson's disease, multiple sclerosis, amyotrophic lateral sclerosis, progressive supranuclear palsy, epilepsy, Creutzfeldt-Jakob disease, AIDS-related dementia, familial infantile convulsions, paroxysmal chorecathetosis, psychiatric disorders such as depression, anxiety, schizophrenia, psychoses, mania or phobic disorders, learning or memory disorders such as ammesia, age-related memory loss, or a neurological disorder such as ampasia, age-related are also useful to treat a pain disorder. The present sequence represents the coding sequence of the human TLCC-2 polypeptide.
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                                                                                                                                                                                                                          New nucleic acid designated TLCC-2 encodes a transient receptor potential-like calcium channel and is useful to diagnose and treat pain disorders and central nervous system neurodegenerative and neurological
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1416 CATGTTTGTGACGTTCGCCGCCATGCAGGCGCAGCAGGCCCGCAGCAGCAGCGTGTGTGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70.8%; Score 142.4; DB 24; Length 1740; 99.3%; Pred. No. 1.7e-28; tive 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human TRP-like calcium channel TLCC-2 coding sequence #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1740 BP; 319 A; 578 C; 475 G; 368 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1476 criciccascriciaccriracic 1499
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1, Fig 1A-B; 70pp; English.
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Curtis RAJ, Silos-Santiago I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 143; Conservative
                                                                                              WPI; 2002-338931/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                      P-PSDB; ABB07816
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WO200153312-A1

26-JUL-2001

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CATGITIGIACGITCGCCGCCAIGCAGGCGCAGCAGCGCGCAGCAGCCTGGTGTGGCT 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             disorders, including central nervous system disorders such as Alzheimer's, Parkinson's and Huntington's diseases, multiple sclerosis, Gilles de la Tourette's syndrome, autonomic function disorders, learning or memory disorders, pain disorders and disorders of cellular proliferation, including cancer. The present sequence is the TLCC-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to the protein and coding sequences of human transient receptor potential (TRP)-like calcium channel protein-2 (TLCC-2). The sequences can be used in the treatment of TLCC-2 related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amnesia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Humnostatic; amyotrophic lateral sclerosis; SNy-brager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel isolated human transient receptor potential-like calcium channel
protein-2 useful for treating Alzheimer's disease, depression, amnesia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58 GCAGTTCCGCTCACCTCTCCATGGTGTCTGAGTGCCTGTTCTCGCTCATCAATGGGGACGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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                            "Trcc-2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Fig 1; 148pp; English
                                                                                                                                                                                                                                                                                                                                                                                             Curtis RAJ, Silos-Santiago I;
                                                                                                                                                                                                                        06-APR-2001; 2001WO-US11442
                                                                                                                                                                                                                                                                               07-APR-2000; 2000US-0544797
                                                                                                                                                                                                                                                                                                                                      (MILL-) MILLENIUM PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pain disorder, and cancer -
/*tag= a
/product=
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                                                         partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       143; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-010913/01.
P-PSDB; AAM51858.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              coding sequence
                                                                                                             WO200177331-A1
                                                                                                                                                                    18-OCT-2001.
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AAI59236
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The invention relates to human nucleic acids (AAI57798-AA161369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polymorlectides are useful in gene therapy. A composition containing a polypeptide or polymorlectide of the invention may be used to treat diseases of the peripheral neuropaths of the invention may be used to treat diseases of the peripheral neuropaths and central neurous system diseases, such as peripheral neuropaths and central neuropaths and localised neuropathies and central nervous system diseases, such as a lateral solerosis, and Shy-Drager Syndrome. Other uses include the cuilisation of the activity search Syndrome. Other uses include the cuilisation of the activity, chemotactic/chemokinetic activity, haemostatic and thrombolyric activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and contributed the printed contributed and the part of the printed contributed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wang D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58 GCAGTICCGCICACTCTCCATGGTGTCTGAGTGCCTGTTCTCGCTCAATGGGGACGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Qian XB, Ren F, V
Yang Y, · Zhang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 70.8%; Score 142.4; DB 22; Length 1741; Best Local Similarity 99.3%; Pred. No. 1.7e-28; Matches 143; Conservative 0; Mismatches 1; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nen R, Ma Y, (
tu C, Xue AJ,
Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 1439; 10078pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1272 circiccagciciacciinacic 1295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chen R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         178 CTTCTCCCAGCTCTACCTC
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Wehrman T, Xu
Goodrich R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAF81753 standard; cDNA; 2052 BP
                                                                                                                                                                                  2000US-0488725.
2000US-0552317.
2000US-0598042.
2000US-0620312.
                                                                                                                                                                                                                                                                                                       2000US-0653450.
                                                                                                                     26-DEC-2000; 2000WO-US34263
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2000US-0727344.
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Wang Z, W
Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; AAM40080
                                                                                                                                                                                                                                                                                                       03-AUG-2000;
14-SEP-2000;
19-OCT-2000;
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                                                                                                                                                                                                                                           09-JUL-2000;
                                                                                                                                                                                  21-JAN-2000;
25-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                    29-NOV-2000;
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Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YT,
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PART BARRER BARR
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à g Homo sapiens

leukaemia;

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Isolated polypeptide with a human membrane associated protein sequence is useful for the diagnosis, prevention and treatment of cell proliferative, autoimmune/inflammatory, neurological and
                    Human, membrane associated protein, MEWAP, diagnosis, cytostatic, antiinflammatory, anticonvulsant, immunosuppressive, antidiarrheic, antiarteriosclerotic, gene therapy, cell proliferative disorder, autoimmune disorder, inflammatory disorder, neurological disorder, gastrointestinal disorder, cencer, inflammation, atherosclerosis, epilepsy, diarrhoea, ss.
                                                                                                                                                                                                                                             Tang YT, Bandman O, Burford N, Azimzai Y;
 Human membrane associated protein MEMAP-13 encoding cDNA
                                                                                                                                                                                                                                                                                                                                                                   Claim 5, Page 157-158; 173pp; English.
                                                                                                                                                                                                                                                         Patterson C;
                                                                                                                                                                                       99US-0149641.
99US-0164203.
                                                                                                                                                                  14-AUG-2000; 2000WO-US22315.
                                                                                                                                                                                                                         (INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                                                                                                                                                                                              gastrointestinal disorders -
                                                                                                                                                                                                                                              Yue H, Tang
R, Lu DAM,
                                                                                                                                                                                                                                                                               WPI; 2001-168860/17.
                                                                                                                                                                                                                                                                                         P-PSDB; AAB74707
                                                                                                                       WO200112662-A2.
                                                                                                                                                                                         17-AUG-1999;
09-NOV-1999;
                                                                                                                                              22-FEB-2001
                                                                                                                                                                                                                                                         Baughn MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          with MEMAP
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MEMAP) given in AABF4777 encode the human membrane associated proteins (MEMAP) given in AABF4695 to AAB74731. MEMAPS have cytostatic, antidinflammatory, antidorulisant, immunosuppressive, antidiarrheic and antidorulisant, immunosuppressive, antidiarrheic and antidorulisant, immunosuppressive, antidiarrheic and associated with decreased expression of functional MEMAP are used to treat a disease or condition associated with overexpression of functional MEMAP. These disorders include cell proliferative, autoimmune/inflammatory, neurological and gastrointestinal disorders. The MEMAP polyuncleotides and proteins are also used for the diagnosis of these disorders. Specific examples of these disorders include cancer, inflammation, atherosclævois, epilepsy and diarrhoea. MEMAP proteins can be used to screen for compounds which specifically bind MEMAP including antibodies, oligonucleotides, proteins and small molecules. MEMAP polyuncleotides can be used to prepare transgenic animals which can be studied to provide information concerning human disease. Anti-MEMAP antibodies are useful in immunoassays for the detection of MEMAP protein and can be used as antagonists to treat or prevent a disorder associated with MEMAP. Purple disorder associated with MEMAP. Purple disorder associated with meman can be delivered to target cells with genetic abnormalities with respect to the expression of MEMAP to treat or prevent a disorder associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1463 GAAGITCCGCICACTCTCCAIGGTGTCTGAGTGCCTGTTCTCGCTCATCAATGGGACGA 1522
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58 GCAGTTCCGCTCACTCTCCATGGTGTCTGAGTGCCTGTTCTCGCTCATCAATGGGGACGA 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         118 CATGITIGIACGITCGCCGCCATGCAGGCGCAGGCCGCAGCCAGCAGCCTGGTGTGCCT 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 22; Length 2052;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2052 BP; 375 A; 670 C; 582 G; 425 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 1.8e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70.8%; Score 142.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 143;
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1463 GAAGTTCCGCTCACTCTCCATGGTCTCTGACTGCTCTTCTCGCTCATCATGGGGACGA 1522

178 CTTCTCCCAGCTCTACCTTTACTC 201

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The invention relates to novel genes (ABL89449-ABL90853) and proteins (ABB89040-ABB90444) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune chaemodyric anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumaroid arthritis and ulcerative colitis; (c) cardiovascular disorders such as mycoardial ischaemias; epilepsy, and (f) infectious diseases such as viral, bacterial, fungal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58 GCAGTICCGCTCACTCTCCAIGGTGTCTGAGTGCCTGTTCTCGCTCATCAATGGGGACGA 117
                                                                                                                                                                                                                                                                                       Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; unnearay; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel 1405 isolated polypeptides, useful for diagnosis, treatment and prevention of neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 24; Length 2092;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 4; SEQ ID NO 920; 2081pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 142.4; DB 24; pred. No. 1.88-28; I. Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2092 BP; 399 A; 676 C; 590 G; 425 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
1583 CTTCTCCCAGCTCTACTC 1606
                                                                                                                                                                                                                                                     Human polynucleotide SEQ ID NO 920.
                                                                                                                            ABL90358 standard; cDNA; 2092 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HUMA-) HUMAN GENOME SCI INC.
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Best Local Similarity 99.3%;
Matches 143; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-MAY-2000; 2000US-205515P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-MAY-2001; 2001WO-US16450.
                                                                                                                                                                                                                24-MAY-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and parasitic infections.
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P-PSDB; ABB89949.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200190304-A2.
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expressed in. Examples of the activities are: cytostatic; anti-proliferative; immunosuppressive; antibacterial; and vulnerary. The secreted proteins and their related polymucleotide sequences are useful for diagnostic and therapeutic methods useful for diagnostic and therapeutic methods useful for diagnosing and treating disorders related to the secreted proteins. The proteins, and polymucleotide sequences may be useful for treating disorders of the immune system, hyperproliferative disorders, infectious disease, regeneration of tissues, for chemotaxis and for screening molecules that bind to the proteins. The proteins or polymucleotide sequences may be used as food additives or preservatives, to increase or decrease storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The polynucleotide sequences given in AAA39052 to AAA39088 encode the human secreted proteins given in AAB08891 to AAB08984. The human secreted proteins can have activities based on the tissues and cells they are
118 CATGITIGIGACGITCGCCGCCATGCAGGCGCAGCAGGCCGCAGCAGCTGGTGGTGTGT 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, co-factors or other nutritional components. Agonists or antagonists of the proteins may be used to prevent scar tissue growth during wound healing, and hyper-vascular diseases. AAA39943 to AAA39051 and AAB088890 are sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                      Human, secreted protein, cytostatic; anti-proliferative, vulnerary, immunosuppressive, antibacterial, diagnosis, immune system, chemotaxis, hyperproliferative disorder; infectious disease; tissue regeneration, screening; food additive; preservative, wound healing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human secreted proteins and coding sequences useful in diagnostic and therapeutic methods for disorders such as immune system or proliferative disorders, related to the proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NI. J.
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                                                                                                                                                                                                                                                                                                                                                     Human secreted protein gene 16 SEQ ID NO:26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ruben sM, Rosen CA, Duan RD, Shi Y, Komatsoulis G, Endress GA, Soppet DR;
                                                                                                          1583 CTTCTCCCAGCTCTACCTTTACTC 1606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 331-332; 416pp; English.
                                                                                  178 CITCICCCAGCICIACCITIACIC 201
                                                                                                                                                                                                                              AAA39067 standard; cDNA; 2094 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HUMA-) HUMAN GENOME SCI INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-0102895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hyper-vascular disease; ss.
                                                                                                                                                                                                                                                                                                            (first entry)
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P-PSDB; AAB08906.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
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                                                                                                                                                                                                                                                                                                              30-AUG-2000
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                                                                                                                                                                                                                                                                       AAA39067;
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70.8%; Score 142.4; DB 21; Length 2094;

Query Match

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                                                                                   1463 GAAGTTCCGCTCACTCTCCATGGTGTCTGAGTGCCTGTTCTCGCTCATCATGGGGACGA 1522
                                                                                                                                                           1523 carerriergacerreecceccarecadececacecaceccecaceaccaceaccaceaccacerecaca 1582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a novel transient receptor potential (TRP)-like calcium channel, designated TLCC-2 and polynucleotides encoding the TLCC-2. TLCC-2 can be expressed by standard recombinant methodology. The TLCC-2 polypeptide, polynucleotides and modulators are useful for treating central nervous system disorders such as neurodegenerative disorders for example Alzheimer's disease, Parkinson's disease, multiple solerosis, amyortrophic lateral solerosis, progressive supranuclear palsy, epilepsy, Creutzfeldt-Jakob disease, AlDS-related dementia, familial infancile convulsions, paroxysmal chorecathetosis, psychiatric disorders such as depression, anxiety, schizophrenia, psychoses, mania or phobic
                                                     117
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transient receptor potential like calcium channel; TRP; TLCC-2; human; neuroprotective; analgesic; nootropic; antiparkinsonian; antidepressant; cerebroprotective; anxiolytic; antimanic; anticonvulsant; gene therapy; calcium signaling; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid designated TLCC-2 encodes a transient receptor potential-like calcium channel and is useful to diagnose and treat pain disorders and central nervous system neurodegenerative and neurological
                                                       58 GCAGTTCCGCTCACTCTCCATGGTGTCTGCTGCCTGTTCTCGCTCATCAATGGGGACGA
                                                                                                                             118 CATGITIGIGACGITCGCCGCCATGCAGGCGCCAGCAGCAGCAGCAGCCTGGTGTGGCT
                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "transient receptor potential-like calcium channel"
                    0
                    Indels
   Pred. No. 1.8e-28;
                  0; Mismatches
                                                                                                                                                                                                                                       1583 CTTCTCCCAGCTCTACCTTTACTC 1606
                                                                                                                                                                                                     178 CTTCTCCCAGCTCTACCTTTACTC 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
141..1883
                                                                                                                                                                                                                                                                                                                                                                                                                                         Human TLCC-2 protein encoding cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product= "TLCC-2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Fig 1A-B; 70pp; English.
                                                                                                                                                                                                                                                                                                                                ABL40754 standard; cDNA; 2095 BP.
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99.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                        Matches 143; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-338931/37.
P-PSDB; ABB07816.
     Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                  ABL40754;
                                                                                                                                                                                                                                                                                            RESULT 12
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1556 CATGTTTGTGACGTTCGCCGCATGCAGGGCGCAGCAGCAGCAGCAGCCTGGTGTGCCT 1615
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                                                                                                                                                                                                                           1496 GAAGTICCGCTCACTCTCCATGGTGTCTGAGTGCCTGTTCTCGCTCATCAATGGGGGACGA 1555
disorders, learning or memory disorders such as amnesia, age-related memory loss, or a neurological disorder such as migraine. The molecules are also useful to treat a pain disorder. The present sequence represents a cDNA encoding the human TLCC-2 polypeptide.
                                                                                                                                                                                            58 GCAGTTCCGCTCACTCTCCATGGTGTCTGAGTGCCTGTTCTCGCTCATCAATGGGGACGA 117
                                                                                                                                                                                                                                                            118 CATGITTGIGACGITCGCCGCCAIGCAGGCGCAGGGCCGCAGCCAGCCTGGIGIGGCT 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to the protein and coding sequences of human transient receptor potential (TRP)-like calcium channel protein-2 (TLCC-2). The sequences can be used in the treatment of TLCC-2 related disorders, including central nervous system disorders such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nociception; nootropic; neuroprotective; antiparkinsonian; cytostatic; hypotensive; antidepressant; analgesic; anticonvulsant; tranquiliser; Parkinson's disease; multiple sclerosis; Gilles de la Tourette's syndrome; autonomic function disorder; neuroleptic; gene therapy; Alzheimer's disease; CNS disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel isolated human transient receptor potential-like calcium channel protein-2 useful for treating Alzheimer's disease, depression, amnesia
                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; TLCC-2; TRP-like calcium channel; membrane excitability;
                                                                                                                                                          0
                                                                                                                       DB 24; Length 2095;
                                                                                                           Score 142.4; DB 24; Lucy Pred. No. 1.8e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human TRP-like calcium channel TLCC-2 coding sequence #1.
                                                                                     Sequence 2095 BP; 388 A; 682 C; 594 G; 431 T; 0 other;
                                                                                                           70.8%; scc...
99.3%; Pred. No. ...
0; Mismatches
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141.,1883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product= "TLCC-2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAI71699 standard; cDNA; 2095 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Silos-Santiago I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MILL-) MILLENIUM PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-APR-2000; 2000US-0544797
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pain disorder, and cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                          143; Conservative
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                                                                                                                      Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAI71699;
                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                     AAI71699
SXCCCC
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Alzheimer's, Parkinson's and Huntington's diseases, multiple sclerosis, Gilles de la Tourette's syndrome, autonomic function disorders, learning or memory disorders, pain disorders and disorders of cellular proliferation, including cancer. The present sequence is the TLCC-2 coding sequence including the 3' UTR.
                                                                                                                                                                                                                                               58 GCAGTTCCGCTCACTCTCCATGGTGTCTGAGTGCCTGTTCTCGCTCATCAATGGGGACGA
                                                                                                                                                                                                                                                                                                                                                               1556 CATGTTTGTGACGTTCGCCGCCATGCAGGCGCAGCAGGCCCGCAGCAGCTGTGGCT
                                                                                                                                                                                                                                                                                   1496 GAAGITCCGCTCACTCTCCATGGTGTCTGAGTGCCTGTTCTCGCTCATCAATGGGGGACGA
                                                                                                                                                                                                                                                                                                                           118 CATGTTTGTGACGTTCGCCGCCATGCAGGCGCAGCAGGCCCGCAGCAGCCTGGTGTGCCT
                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                 DB 24; Length 2095;
                                                                                                                                                                                                       ;
0
                                                                                                                                                              ch 70.8%; Score 142.4; DB 24; Length l Similarity 99.3%; Pred. No. 1.8e-28; Conservative 0; Mismatches 1; Indels
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                                                                                                                        Sequence 2095 BP; 388 A; 682 C; 594 G; 431 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA encoding novel human diagnostic protein #25122.
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                                                                                                                                                                                                                                                                                                                                                                                                        178 CTTCTCCCAGCTCTACCTTTACTC 201
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23-AUG-2000; 2000US-0649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-639362/73
                                                                                                                                                              Query Match
Best Local Similarity
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                                         disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. Asset197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from MIPO
             and (II) are useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        321 GAAGTICCGCICACICICCAIGGIGICTICAGIGCCIGITCICGCTCATCAATGGGGACGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ren F, W
Zhang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0,
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Yang Y,
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Pred. No. 3.8e-28;
0; Mismatches 2,
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Xu C, Xue AJ,
R, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                     specification, but was obtained in electroni
at ftp.wipo.int/pub/published_pct_sequences.
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Wang Z, Wehrman T, X
Zhou P, Goodrich R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 98.6%;
Matches 142; Conservative
    expressing
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19-JUL-2000; 2000US-0659312.
03-AUG-2000; 2000US-0653450.
14-SEP-2000; 2000US-0693036.
19-OCT-2000; 2000US-0693036.
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2000US-0552317.
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P-PSDB; AAM41866.
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Wang J,
Zhao QA,
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immunosuppressant and cytostatic activity. The polymoclectides are useful in gene therapy. A composition containing a polymeptide or polymuclectide of the invention may be used to tract diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system, such as peripheral nervous injuries, peripheral nervopathy and localised neuropathies and central nervous system diseases, such as Alzheimer's Parkinson's disease, muticon's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         474
                                                                                                                                                                                                                                                                                                                                                                                        Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     533 CATGITITGIGACGITCGCCGCCAIGCAGCCCCAGCAGCCCGCAGCAGCCTGGIGGCC
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                                                                                                                                            The invention relates to human nucleic acids (AAIS7798-AA161369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Gaps
                      Novel nucleic acids and polypeptides, useful for treating disorders
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                                                                                                                                                                        with nootropic
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                                                  such as central nervous system injuries
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Human, immune, haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
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2000US-0180628.
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2000US-0190076
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18-APR-2000; 2
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04-FEB-2000;
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14-JUL-2000; 2000US-02174967.

16-JUL-2000; 2000US-0218290.

26-JUL-2000; 2000US-0220663.

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20-CCT-2000; 2000US-0241808.
20-CCT-2000; 2000US-0241808.
20-CCT-2000; 2000US-0241809.
20-CCT-2000; 2000US-0244617.
08-NOV-2000; 2000US-0246477.
08-NOV-2000; 2000US-0246477.
08-NOV-2000; 2000US-0246477.
08-NOV-2000; 2000US-0246524.
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(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-483426/52

Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -

Disclosure; SEQ ID NO 28638; 3071pp + Sequence Listing; English

AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have eytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome

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Homo sapiens
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that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polymucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polymucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK64922 to AAK64950 and AAM82169 represent sequences used in the exemplification of the present invention.
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11-JUL-2000; 2000US-0217487.
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Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -

Disclosure; SEQ ID NO 28639; 3071pp + Sequence Listing; English.

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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to pupplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, companies and cancer metastases of haematopoietic-derived cells. AAK64703 cancers and cancer metastases of haematopoietic antigen genomic companies from the present invention. AAK84912 to AAK84950 and AAM82169 cell represent invention.
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Best Local Similarity 99.7
Matches 1497; Conservative
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| qq | 4821 (| | 4880 |
|--------------------|------------------------------|--|------|
| Qy | | ACTCCCTGTCCTTAGACTGCATCCAGGTGGATCCCCCGGGGGGCCCCCTCCGCCCCCC 8 | 840 |
| ਰ <u>ਹ</u> | 4881 | CCTGTCCTTAGACTGCATCCAGGTGGGATCCCCCCGGGCCCCCTCCGCCCCCA | 4940 |
| \$ £ | 841 (| GCGACGATCTCACCCTCTTGGAAAGCAGCTCCAGTTACAAGAACCTCACGCTCAAATTCC 9 | 900 |
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| S & | | ACANGIACI GCCI GCT CALLONGO GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG | 960 |
| δλ | 961 | CTCACCCCAGCACTACTTCCCTAAGGTGGGGACAGGGCCCCCCCC | 1020 |
| Dp | 5061 | | 5119 |
| ò | 1021 | CTGCTGGGTGAGCACTTCCCCTGCCAGAGTGCAGAGTGGCAGGGGAGGCTGGC 1 | 1080 |
| OD | 5120 | ACTICCCCTGCCAGCTGCAGACTCAGCACGTGGCAGGGACGCTGG | 5179 |
| ò | 1081 2 | CCTGACCCTCACCCGAGCCTCCTGCCTAGG 1 | 1140 |
| qq | 5180 4 | :CGGAAGGACCCCAAGACGCCCCTGCTCTCTCTCTCTCTCT | 5239 |
| QY DP | 1141 C 5240 C | CTGGTCAATGTCACCATCCACTTCCGGCTGAAGACCATTAACCTCCAGAGCCTCATCAAT 1 | 1200 |
| · Qy | 1201 | () ~ | 1260 |
| g | . 5300 7 | AATGAGATCCCGGACTGCTATACCTTCAGCGTCCTGGTGAGGCCCCCCGGGAACCCAAG | 5359 |
| Qy | 1261 | GGCTCCTGAGTTCCAGGGACCTGGTCAGGGAGTGTCTTGGGAGCACTGGCCAAGG 1 | 1320 |
| qq | 5360 (| Ŋ | 5418 |
| ò | н | GCAAGCGTGCGGGTGATGAGGGAGGGAGCCCGGGGTCTGTCAGGCCACCTGTCATGTGGA 1. | 1380 |
| QQ | 5419 | വ | 5478 |
| 07 | 1381 C | CITGGGGCTTGGGGTCAAGGTTTACTCTGCCCCCAAGGCCCCCACAGATCACGT 1 | 1440 |
| DÞ | 5479 (| CTTGGGGCTTGGGGCTGCCAAGGTTTACTCTGCCCCCAACTGGCCCCCACAGAGATCACGT 5 | 5538 |
| δλ | 1441 | CCTGGAGACCCAGGCCCACATCC 1 | 1500 |
| QQ | 5539 7 | CAACAAAGCACCACAGTGGGCGGATCCCCATCAGCCTGGAGACCCAGGCCCACATC | 5598 |
| δλ | 1501 A | 1501 | |
| QQ | 5599 7 | . 5599 | |
| RESU AAS6 ID | ULT 3 65931 AAS65931 s | tandard; cDNA; 776 BP. | |
| Y X | 36593 | | |
| X E S | 13-FEB-200 | 2 (first entry) | |
| DE X | DNA encodi | ng novel human | |
| XX | Human; chr food suppl | omosome mapping, gene mapping, gene therapy, forensic, ement, medical imaging, diagnostic, genetic disorder, ss. | |
| SO | Homo sapie | ns. | |
| A W X | WO20017506 | 7-22. | |

11-0CT-2001

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AAK67282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in the printed and to produce other types of data and products dependent on DNA and and to produce other types of data and products dependent on DNA and and and to produce other types of the invention of assess by indiversity and to produce data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO specification.
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                                                                                                                                                                                                                                                                                                                   New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID No 1735; 103pp; English.
                                                                                                                                                                                                          Tang YT;
                                              30-MAR-2001; 2001WO-US08631.
                                                                                       31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
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AAK67282 standard; DNA; 33147 BP.

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Human, immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
                          Human immune/haematopoietic antigen genomic sequence SEQ ID NO:22094
                                                                                     17-JAN-2001; 2001WO-US01354.
                                                                                                                                                                                                                000US-0225214
                                                                                                                                                                                                                          000US-0225267
000US-0225268
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                                                                                                                           2000US-0190076
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               06-NOV-2001 (first entry)
                                                                WO200157182-A2.
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06-SEP-2000;
06-SEP-2000;
                                                      Homo sapiens.
                                                                                                                                18-APR-2000;
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14-SEP-2000; 2000US-0233063.
14-SEP-2000; 2000US-0233064.
14-SEP-2000; 2000US-0233064.
21-SEP-2000; 2000US-0234223.
21-SEP-2000; 2000US-0234274.
25-SEP-2000; 2000US-0234999.
26-SEP-2000; 2000US-0234999.
                                                                                                                                                                                                                                                                                                                                                                                2000US-0256719
                                                   27-SEP-2000; 2
27-SEP-2000; 2
29-SEP-2000; 2
                                                                                      02-OCT-2000;
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02-OCT-2000;
13-OCT-2000;
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.6496 GGCACCTGTAGTCCCAGCTACTCGGGAGGCTGAGGAATCACCTGAACCTGGGGG 16555
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16316 AGAGACAGCCATGAAGATAACTAGCTGAGGCCAGGTACAGTGGCTCATGCCTATAATCCC 16375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to polynucleotides may be used to product on (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        unaguose and treat immune/haematopoietic-related diseases, especially canners and cancer metastases of haematopoietic-derived calls. AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAM82169 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              478 GITGAGGCTGCAGTAAGCTATGACCACGCTGCTGCACTCCACCCTGGGTGACAGAGTGAG 537
                                                                                                                                                                                                                                                                                                                                                               Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16436 AATAACATAGCAAAACCCCATCCCTACTAAAATACAAAATTAGCTGGGCGTGGTGGTGGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure, SEQ ID NO 22094; 3071pp + Sequence Listing; English
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Best Local Similarity 77.5%; Pred. No. 1.9e-40;
Matches 268; Conservative 0; Mismatches 75; Indels 3;
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2000US-0251868.
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               08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
11-DEC-2000;
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AAD52898 standard; DNA; 47999 BP

RESULT 5 AAD52898 ID AAD52

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Human, tweety homologue 2, TTYH2, therapy, cancer, tumour, cytostatic, diagnostic marker, gene; ds.
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product= "Human TTYH2 protein"
                                     Human tweety homologue 2 (TTYH2) gene.
                                                                                         location/Qualifiers
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19377..39562
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8903..28975
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                      14-MAY-2003 (first entry)
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                                                                            Homo sapiens.
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18377 AATAAGATCAATAGCTTAAGTTGAGTGTGGGGGTCACGCCTGAAATCCCAGCACTTTGG 18436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           251 ATTAAAATCAACAGCTGTGGCTGGGCACGGTGGCTCACGCCTATAATACCAGCACTTTGG 310
                                                                                                                                                                                                                                                                                                                                                                                                                               New human tweety homolog 2 polypeptides and polynucleotides, useful for producing an antigen-binding molecule that is immuno-interactive with the polypeptide or as diagnostic markers for cancers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       371 GAAGACCTTGTCTCTACGCACA-----AACAAATTAGCTGGGCGTGGTGGCGGTGCC
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Best Local Similarity 79.3%; Pred. No. 3.9e-40;
Matches 264; Conservative 0; Mismatches 60; Indels 9;
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                                                                                                                                                                                                                                                        14-MAY-2002; 2002WO-AU00591
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                 intron
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Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
                                               Human immune/haematopoietic antigen genomic sequence SEQ ID NO:37304.
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2000US-0225447.
2000US-0225757.
2000US-0225757.
                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-0231414.
2000US-0232080.
2000US-0232081.
                                                                                                                 17-JAN-2001; 2001WO-US01354
                                                                                                                                                                                                                                                                                                                             2000US-0226868
                                    07-NOV-2001 (first entry)
                                                                                          WO200157182-A2.
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05-SEP-2000,
06-SEP-2000,
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08-SEP-2000,
08-SEP-2000,
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08-SEP-2000;
08-SEP-2000;
                                                                              Homo sapiens
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                                                                                                     09-AUG-2001
                        AAK82492;
RESULT 6
AAK82492
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Amino acid sequences given in AMM81210 to AAM91921. (1) have cytostatic activity, and can be used in gene therapy and vaccine production. (1) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (1) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (1) by expression in a patient's genome that affect the activity of (1) by expression for to supplement the patients own produce the secreted (1), by inserting polynucleotides may be used to produce the secreted (1), by inserting protein. (1) proteins and polynucleotides may be used to produce the secreted (1), by inserting protein. (1) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-derived cells. AAK64703 cancers and cancer metastases of haematopoietic antigen genomic to AAX87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK49942 to AAK54500 and AAM82169 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           177 TCACCTGAGGTTAGAAGTTTGAGACCAGCCTGGGCAACATGACAAAACCCCGTCTCTACT 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              297 GCTGAGGCAGAAGAATGGCTTGAACCCAGGAGGTGGAGGTTGCAGTGAGCCAAGATCACA 356
                                                                                                                                                                                                                                                                                                                                                             Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                388 --GCACAAACAAATTAGCTGGGCGTGGTGGCGTGCCCCTGTGGTCCCAGCTACTCAGGAG
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                                                                                                                                                                                                                                                                                           Ruben SM;
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2000US-0251856.
2000US-0251868.
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2000US-0251989.
2000US-0251990.
2000US-0254097.
                                                                                                                                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                05-JAN-2001; 2001US-0259678.
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Best Local Similarity 81.2
Matches 255; Conservative
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01-DEC-2000;
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40714 GGCCGGGCGCAGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGTGGGCAGG 40773
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequence represents a human asthma associated gene (AAGB) genomic DNA sequence. The invention relates to a novel asthma-associated gene AAGB and the polypeptide encoded by AAGB. The polypeptide of the invention has antiinflammatory and antiasthmatic activity, and may have a use in gene therapy, or as a vaccine. The polypeptide, polymotleotide, antibody and antisense oligonucleotide of the invention (collectively referred to as agents) are useful for treating an inflammatory or obstructive airways tisease. They are also useful for are useful for treating adult trespiratory distress syndrome (ARDS), chronic obstructive pulmonary or airways disease (COPD or COAD), including chronic bronchitis or dyspnea associated with it, emphysema, exacerbation of airways hyper-reactivity consequent to other drug therapy and pneumoconiosis. The agents are also useful in the treatment of eosinophil related disorders and asthma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        329 TTGCTTGAGGCCAGAAGTTTGAGACCCAGGCTGGGCCACGTAGGAAGACCTTGTCTCTAC- 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               388 --GCACAAACAAATTAGCTGGGCGTGGTGGCGTGCCCCTGTGGTCCCCAGCTACTCAGGAG 445
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                                                                                                                                                                                            Human; asthma; AAGB; antiinflammatory; antiasthmatic; ARDS; COPD; COAD;
                                                                                                                                                                                                                 inflammatory disease; obstructive airways disease; dyspnea; emphysema; adult respiratory distress syndrome; chronic bronchitis; eosinophil; chronic obstructive pulmonary disease; pneumoconiosis; chronic obstructive airways disease; gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel polypeptide encoded by disease associated gene, useful for treating an inflammatory or obstructive airways disease e.g. asthma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56; Indels
                                                                                                                                                      Human asthma-associated gene AAGB genomic DNA #1.
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81.2%; Pred. No. 5.5e-40;
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0; Mismatches
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(NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
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                  ABA98944 standard; DNA; 50000 BP
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                                                                                                          (first entry)
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Best Local Similarity 81.2%
Matches 255; Conservative
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2000US-0241826.
2000US-0241826.
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2000US-0246474.
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2000US-0236370.
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2000US-0246524.
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27-SEP-2000;
29-SEP-2000;
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                                           40894 GCTGAGGCAGAAGAATGGCTTGAACCCAGGAGGTGGAGGTTGCAGTGAGGCCAAGATCACA 40953
                       Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antirheumatic; hepatotropic; cerebroprotective; antiinflammatory; antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal; antiparasitic; cardiant; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
                                                                                                                                                                                                                   Human nervous system related polynucleotide SEQ ID NO 10242.
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ID ABA17911 standard; DNA; 15765
                                                                                           41014 AAAAAAAAAGTATG 41027
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2000US-0209467.
2000US-0214886.
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2000US-0216647.
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2000US-0184664.
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2000US-0224519.
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14-AUG-2000; 2
14-AUG-2000; 3
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The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune discretars e.g. Addison's disease, alleragies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis, (c) cardiovascular discrets such as mycocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections.

Colitis, (c) cardiocardial protein and certification, but was obtained in electronic format directly from WIPO at ftp.wipo.inf/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 10242; 1701pp + Sequence Listing; English.
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                                                                                                                                             2000US-0249264.
2000US-0249265.
2000US-0249297.
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2000US-0249300,
2000US-0250391,
2000US-0251160,
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2000US-0251988.
2000US-0256719.
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2000US-0251990.
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05-JAN-2001; 2001US-0259678.
                                                  2000US-0249215.
2000US-0249216.
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2000US-0249218.
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2000US-0251868.
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                     2000US-0249213
                                                                                                                     2000US-0249244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  useful for preventing, cancers and metastases
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                                                                                                     .7-NOV-2000;
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4064 AAAACCCTGTCTACTAAAAAGTGCAAAATTAGCCGGATATGGTGGTGCACACCTGTA 4005
                                                                                          1004 Arcccadcracrcadedadecrdadedadaarcccrrcaacccadedrdadarrd 3945
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372 AAGACCTIGICICIACGCACAA----ACAAATTAGCTGGGCGTGGTGGCGTGCCCTGTG
                                                               428 GICCCAGCTACTCAGGAGGCTGAGGCAGGAGGATCGCTTGAGTCCGGGAGGTTGAGGCTG
                                                                                                                          488 CAGTAAGCTATGACCACGCTGCTGCACCCCTGGGTGACAGAGTGAGACCCTGTCTC
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07-JUN-2000;
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14-AUG-2000;
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22-AUG-2000; 2000US-0226681.
22-AUG-2000; 2000US-02268681.
23-AUG-2000; 2000US-0227182.
23-AUG-2000; 2000US-0229343.
01-SEP-2000; 2000US-0229343.
01-SEP-2000; 2000US-0229343.
01-SEP-2000; 2000US-0229343.
01-SEP-2000; 2000US-02293445.
05-SEP-2000; 2000US-02293445.
05-SEP-2000; 2000US-02293445.
06-SEP-2000; 2000US-02293445.
08-SEP-2000; 2000US-0231244.
08-SEP-2000; 2000US-0231244.
08-SEP-2000; 2000US-0231244.
08-SEP-2000; 2000US-023144.
08-SEP-2000; 2000US-0231244.
08-SEP-2000; 2000US-0231244.
08-SEP-2000; 2000US-0231244.
08-SEP-2000; 2000US-0231241.
08-SEP-2000; 2000US-0231297.
14-SEP-2000; 2000US-0232397.
14-SEP-2000; 2000US-0232397.
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26-SEP-2000; 2000US-0234998

27-SEP-2000; 2000US-0235834

27-SEP-2000; 2000US-0235834

29-SEP-2000; 2000US-0235836

29-SEP-2000; 2000US-0235836

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29-SEP-2000; 2000US-0235869

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Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system cancers and metastases -
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08-NOV-2000; 2000US-02496613.
17-NOV-2000; 2000US-0249208.
17-NOV-2000; 2000US-0249208.
17-NOV-2000; 2000US-0249210.
17-NOV-2000; 2000US-0249211.
17-NOV-2000; 2000US-0249211.
17-NOV-2000; 2000US-0249211.
17-NOV-2000; 2000US-0249214.
17-NOV-2000; 2000US-0249214.
17-NOV-2000; 2000US-0249218.
17-NOV-2000; 2000US-024929.
17-NOV-2000; 2000US-0251988.
0S-DEC-2000; 2000US-0251868.
                                                                                                                                                                                                                                                                                                                                                          (HUMA-) HUMAN GENOME SCI INC.
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The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rhumancid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and parasitic infections Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly Disclosure, SEQ ID NO 10581; 1701pp + Sequence Listing, English.

Sequence 15765 BP; 4553 A; 3137 C; 3376 G; 4699 T; 0 other;

Query Match 13.9%; Score 208.2; DB 22; Length 15765; Best Local Similarity 79.5%; Pred. No. 4e-40; Matches 260; Conservative 0; Mismatches 63; Indels 4; Gaps

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14-AUG-2000;
14-AUG-2000;
18-AUG-2000;
22-AUG-2000;
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                                                      4124 AGGCTGAGGTGGGCGGATCACCTGAGGTCAGGAGTTTGAGACCAGCCTGGCCAACATGGC 4065
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4184 TGAAAGITIATGIAAATGGCCGGGCACGGTGGCTCACACCTATAATCCCAGCACTTTGGG 4125
                                                                                                                  1064 AAAACCCTGTCTCTACTAAAAAGTGCAAAAATTAGCCGGATATGGTGGTGGTGCACACACTGTA 4005
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                                AGGCTGAGGAGGAAGGATTGCTTGAGGCCAGAAGTTTGAGACCAGCCTGGGCCACGTAGG 371
                                                                                      372 AAGACCTTGTCTCTACGCACAA----ACAAATTAGCTGGGCGTGGTGGCGTGCCCTGTG 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; imunosopipressive; antihiflammatory; anti-HTV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianemic; antiarthritic; cancer; antirheumatic; hepatotropic; cerebroprotective; antihiflammatory; antialabergic; antidiaberic; antihicer; anticonvulsant; antifungal; antiparastic; cardiant; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
                                                                                                                                               GTCCCAGCTACTCAGGAGGCTGAGGCAGGAGGATCGCTTGAGTCCGGGAGGTTGAGGCTG
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2000US-0205467
2000US-0205486.
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2000US-020964.
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2000US-0198123.
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2000US-0246611.
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08-NOV-2000; 28-NOV-2000; 28-NOV-2000; 208-NOV-2000; 208-NOV-2000; 208-NOV-2000; 217-NOV-2000; 217-N
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17-NOV-22000
11-DEC-2000
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05-DEC-2000
05-DEC-2000
06-DEC-2000
06-DEC-2000
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HUMAN GENOME SCI INC (HUMA-)

Barash SC, Ruben SM; Rosen CA,

WPI; 2001-541565/60.

Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system cancers and metastases -

Disclosure; SEQ ID NO 10607; 1701pp + Sequence Listing; English

The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB1678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are solved from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Cronn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and parasitic infections. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Sequence 15765 BP; 4553 A; 3137 C; 3376 G; 4699 T; 0 other;

2000US-0220964

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                                                                        252 TTAAAATCAACAGCTGTGGCTGGGCACGGTGGCTCACGCCTATAATACCAGCACTTTGGG
                                                                                                     4184 TGAAAGTTTATGTAAATGGCCGGGCACGGTCGCTCACACCTATAATCCCAGCACTTTGGG
                                                                                                                                    312 AGGCTGAGGAGGAAGGATTGCTTGAGGCCAGAAGTTTGAGACCAGCCTGGGCCACGTAGG
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                                          4; Gaps
           Length 15765;
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                                        Indels
         DB 22;
        Score 208.2; DB 22;
Pred. No. 4e-40;
0; Mismatches 63;
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2000US-0198123.
2000US-0205515.
2000US-0205467.
2000US-0215135.
2000US-0216477.
        13.9%;
79.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
Query Match
Best Local Similarity 79.5'
Matches 260; Conservative
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17-MAR-2000;
18-APR-2000;
19-MAY-2000;
07-JUN-2000;
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(HUMA-) HUMAN GENOME SCI INC. useful for preventing, di WPI; 2001-541565/60. Rosen CA,

Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system

Disclosure, SEQ ID NO 11340; 1701pp + Sequence Listing, English.

The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB1678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune disorders acidisease, multiphe. Scherosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological disease e.g. cerebral anoxia and parasitic infections.

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2000US-0240960.
2000US-0241221.
2000US-0241785.
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02-OCT-2000; 2
02-OCT-2000; 2
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1-SEP-2000;
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ulcerative colitis; infection, Hirschsprung's disease, chronic colitis,
digestive system disorder, Meckel's diverticulum; ds.
Note: The Sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                               4; Gaps
                                                                                                                                                                                                       13.9%; Score 208.2; DB 22; Length 15765; 79.5%; Pred. No. 4e-40; Artive 0; Mismatches 63; Indels 4; (
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                                                                                                                                     Sequence 15765 BP; 4553 A; 3137 C; 3376 G; 4699 T; 0 other;
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04-FEB-2000; 2000US-0180628.
02-MAR-2000; 2000US-018664.
03-MAR-2000; 2000US-0189874.
17-MAR-2000; 2000US-0189123.
19-MAY-2000; 2000US-018123.
19-MAY-2000; 2000US-029467.
28-JUN-2000; 2000US-0214886.
30-JUN-2000; 2000US-0216647.
07-JUL-2000; 2000US-0216647.
11-JUL-2000; 2000US-0216880.
11-JUL-2000; 2000US-0216880.
11-JUL-2000; 2000US-0216880.
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Matches 260; Conservative
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The present invention provides the protein and coding sequences of a number of human digestive system antigens. These can be used in the diagnosis, treatment and prevention of digestive system disorders, including cancer, Meckel's diverticulum, bacterial or parasitic infections, appendialitis, Hirschaptung's disease, chronic colitis or ulcerative colitis. The present sequence is a genomic DNA fragment encoding a digestive system antigen of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polynucleotides encoding digestive system antigens, useful for diagnosing, treating, preventing and/or prognozing disorders of the digestive system, particularly cancer and cancer metastases -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 3221; 986pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rosen CA, Barash SC, Ruben SM;
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17-NOV-2000; 2000US-0249214.
17-NOV-2000; 2000US-0249215.
17-NOV-2000; 2000US-0249216.
17-NOV-2000; 2000US-0249244.
17-NOV-2000; 2000US-0249245.
17-NOV-2000; 2000US-0249265.
17-NOV-2000; 2000US-0249267.
17-NOV-2000; 2000US-0249267.
17-NOV-2000; 2000US-0249297.
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2000US-0256719.
2000US-0251479.
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17837 GGCTGGGCACAGTGGCTCCTGCATATAATCCCAGCATCTTTGGGAGGCCCGAGGCAAGAGA 17778
                                                                    17777 TCACTTGAGGCCAGGAGTTCAAGACTAGCCTAGGCAATATAGGAAGACCCTGCCTCTAAA 17718
                                                                                                              17117 AAATTAAAATTAGCCAGGTATGGTGGCCTGTACCTGTAGTCCCAGGTACTAGTCGAGGGCT 17658
                                                                                                                                                             17657 GAGGTAGGAGGATCACTTGAGCCCAGGAATTTGAGGCTGTAGTGAGCTATGATTGTACCA 17598
                                                                                          448
                                            329 TIGCTIGAGGCCAGAAGITIGAGACCAGGCCTGGGCCACGTAGGAAGACCTTGTCTCTACG 388
                                                                                                                                       449 GAGGCAGGAGGATCGCTTGAGTCCGGGAGGTTGAGGCTGCAGTAAGCTATGACCACGCTG 508
389 CACAAACAAATTAGCTGGCGTGGTGGCGTGCCCTGTGGTCCCAGCTACTCAGGAGGCT
                                                                                                                                                                                     Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
                                                                                                                                                                                                                                                                                                                                                                                     Human immune/haematopoietic antigen genomic sequence SEQ ID NO:28037.
                                                                                                                                                                                                                                                                                                                                                                                                                       cytostatic; gene therapy; vaccine; metastasis; ds
                                                                                                                                                                                                                                                        17537 AATCCATATIGTTAAAT 17521
                                                                                                                                                                                                                                                                                                                 AAK73225 standard; DNA; 9359 BP
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2000US-0180628.
2000US-0184664.
2000US-0186350.
2000US-0189874.
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2000US-0220964.
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2000US-0209467
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14-AUG-2000; 2
14-AUG-2000; 2
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18-MAR-2000;
18-MAY-2000;
07-JUN-2000;
28-JUN-2000;
07-JUL-2000;
07-JUL-2000;
11-JUL-2000;
11-JUL-2000;
14-JUL-2000;
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AAX54951 to AAX64702 encode the human immune/haematopoietic antigen (I)

amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic

activity, and can be used in gene therapy and vaccine production. (I)

proteins and polynucleotides may be used in the prevention, diagnosis and

treatment of diseases associated with inappropriate (I) expression. For

example, they may be used to treat disorders associated with decreased

expression by rectifying mutations or deletions in a patient's senome

that affect the activity of (I) by expressing inactive proteins or to

supplement the patients own production of (I). Additionally, (I)

co supplement the patients own production of (I). Additionally, (I)

co polymucleotides may be used to produce the secreted (I), by inserting

the nucleic acids into a host cell and culturing the cell to express the

corrects and treat immune/haematopoietic-related diseases, especially

cancers and cancer metastases of haematopoietic antigen genomic

to AAX87694 represent human immune/haematopoietic antigen genomic

sequences from the present invention. AAX64942 to AAX64950 and AAM82169

corrected to the present invention. AAX64942 to AAX64950 and AAM82169

corrected to the present invention. AAX64942 to AAX64950 and AAM82169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 28037; 3071pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ruben SM;
                                                                                                     2000US-0249209.
2000US-0249210.
2000US-0249211.
2000US-0249212.
2000US-0249213.
2000US-0249213.
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2000US-0249217
2000US-0249241
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2000US-024929
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                                         2000US-0246611.
2000US-0246613.
2000US-0249207.
2000US-0249208.
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2000US-0250391.
2000US-0251030.
2000US-0251988.
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2000US-0251479.
2000US-0251856.
2000US-0251868.
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01-DEC-2000; 2
05-DEC-2000; 2
05-DEC-2000; 2
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08-DEC-2000; 2
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Gaps

Query Match 13.8%; Score 207.8; DB 22; Length 9359; Best Local Similarity 77.1%; Pred. No. 4.2e-40; Matches 266; Conservative 0; Mismatches 77; Indels 2;

Sequence 9359 BP; 1726 A; 2741 C; 3065 G; 1827 T; 0 other;

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07-JUL-2000; 2000US-0216647
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              comprising
              235 AGCCTGAGCTGCTGGGATTAAAATCAACAGCTGTGGCTGGGCACGGTGGCTCACGCTAT 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human, prostate cancer, cytostatic, carcinogen, pharmacodyanamic marker,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer -
                                   7268 AACCCCACATTCCGGCAATCTGTAGAGCTCTTCAGGCCAGGCGCATTGGCTCATGCCTGT
                                                             295 AATACCAGCACTTTGGGAGGCTGAGGAAGGATTGCTTGAGGCCAGAAGTTTGAGACC
                                                                                    7328 AATCCCAGCACTTTGGAAGGCTGGGGGGGGGATCACTTGAGCCCAGGAGTTCAAGACC
                                                                                                                                                             413 TGGCGTGCCCCTGTGGCTCCCAGCTACTCAGGAGGCTGAGGCAGGAGGATCGCTTGAGTCC
                                                                                                                                                                                                               473 GGGAGGTTGAGGCTGCAGTAAGCTATGACCACGCTGCTGCACTCCACCCTGGGTGACAGA
                                                                                                              AGCCTGGGCCACGTAGGAAGACCTTGTCTCTACGCACA--AACAAATTAGCTGGGCGTGG
                                                                                                                                                                                     7448 TGGCTTGTGCCTGTCGTCCCAGCTACTCAGGAGGCTGAGGCGGGGAGGATCGCTTGAACCC
                                                                                                                                                                                                                                     P508 AGGAAGAGGAAGCTGCAGTGAGCCAACATCACGCCACTGCACTCCAGTCTGGGTGACAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an isolated nucleic acid molecule (I) comp a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of th specification or its complement. (I) is useful for: (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient.
                                                                                                                                                                                                                                                                                    7568 GGGAGACCCTGACTCAAAAAAAAAAAAAAAAAAAAAGGAAAGGAA 7612
                                                                                                                                                                                                                                                             Human prostate expression marker cDNA 44762.
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                                                                                                                                                                                                                                                                                                                                                 ABV44771 standard; cDNA; 566
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2000US-207454P.
2000US-211314P.
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2000US-255281P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                362 AAATTCAGCGAGCAGACCGGGCACAGTGGCTCACGCCCATAATCCCAACAGTTGGGGAGG 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTGAGGAGGAAGGATTGCTTGAGGCCAGAAGTTTGAGACCAGCCTGGGCCCACGTAGGAAG 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            375 ACCTTGTCTCTACGCACAAACAAATTAGCTGGGGGGTGGGGGGTGCCCCTGTGGTCCCAG 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCATAATCATACCGCTGCACTCCAGCCTGGGCGACAGAGCAAACTCTGCCTCAAAAACA 63
(d) assessing the efficacy of a therapy for inhibiting prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
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                                                                                                                                                                                                                               (I) is also useful as a pharmacodyanamic or pharmacogenomic marker
                                                                                                                                                                                                                                                                                                                                                                DB 23; Length 566;
                                                                                                                                                                                                                                                                                                                             Score 207.6; DB 25,
pred. No. 1.7e-40;
-hos 74; Indels
                                                                                                                                                                                                                                                                                                 Sequence 566 BP; 134 A; 136 C; 136 G; 160 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 77.3%;
Matches 252; Conservative
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2000US-0217487.
2000US-0217496.
2000US-0218290.
2000US-0220963.
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2000US-0224518.
2000US-0224519.
                                          2000US-0225213
2000US-0225214
2000US-022526
2000US-022526
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2000US-022547
2000US-0225457
2000US-0225757
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2000US-0230437.
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2000US-0241787.
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                    26-JUL-2000;
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14-AUG-2000;
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29-SEP-2000;
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Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
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                              08-NOV-2000; 2000US-0246475.

08-NOV-2000; 2000US-0246476.

08-NOV-2000; 2000US-0246477.

08-NOV-2000; 2000US-0246477.

08-NOV-2000; 2000US-0246523.

08-NOV-2000; 2000US-0246524.

08-NOV-2000; 2000US-0246524.

08-NOV-2000; 2000US-0246527.

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08-NOV-2000; 2000US-0246652.

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2000US-0249207.
2000US-0249208.
2000US-0249209.
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2000US-0249214.
2000US-0249215.
2000US-0249215.
20-0CT-2000; 2000US-0241809
20-0CT-2000; 2000US-0241826
01-NOV-2000; 2000US-0244617.
08-NOV-2000; 2000US-0246474.
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2000US-0249211
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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I)

Disclosure; SEQ ID NO 40838; 3071pp + Sequence Listing; English.

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32083 GCTACTCGGGAAGCTGAGGCAGAGAATCGCTTGAACCCGGGAGGTGGAGGTTGCAGTGA 32024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32261 AAAATTCAAGGGGGAGGCTGGCACGGTGGTGCTCTGTAATACCAGTGCTTTGGGAG 32202
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polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haemacopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703 sequences from the present invention. AAK84942 to AAK87950 and AAM8169 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  254 AAAATCAACAGCTGTGGCTGGGCACGGTGGCTCACGCCTATAATACCAGCACTTTGGGAG 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              314 GCTGAGGAGGAAGGATTGCTTGAGGCCAGAAGTTTGAGACCAGCCTGGGCCACGTAGGAA 373
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13.8%; Score 207.4; DB 22; Length
Best Local Similarity 78.2%; Pred. No. 9.9e-40;
Matches 262; Conservative 0; Mismatches 71; Indels
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Search completed: October 27, 2003, 12:34:11 Job time : 493.838 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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| OM nucleic - n | OM nucleic - nucleic search, using sw model |
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| Run on: | October 27, 2003, 11:10:42; Search time 6013.64 Seconds (without alignments) 10211.014 Million cell updates/sec |
| Title: Perfect score: Sequence: | US-09-851-494B-1_COPY_5500_7000 1501 1 gccggactcacaggccttcgagacccaggcccacatcca 1501 |
| Scoring table: | IDENTITY NUC Gapop 10.0, Gapext 1.0 |

5777422 2888711 seqs, 20454813386 residues Total number of hits satisfying chosen parameters: Searched:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 2000000000

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| SUMMARIES | | Description | 87270 AF287270 Homo | 08878 AC008878 Homo | 21153 AC021153 Homo | 05572S5 AF305576 Homo | 293659 AJ293659 Homo | 05572S4 AF305575 | 05572S3 AF305574 Homo | 20978 AC020978 Homo | 22403 . AC022403 Homo | 59335 Homo | 33695 Homo | 4756 AC084756 Homo | 7501 AC007501 Homo | 10 AC007490 Homo | :0 AC133460 Homo | 96 AC080096 Homo | 17 AX647597 Seque | 3 AC018663 Human | .8 AL663038 Human | 7 AL445467 | .0 AC005210 | 6 AL137066 | '1 AC138071 Homo | 12 AC068682 Homo | AC023283 Homo | 3 AC106753 Homo | AC006057 Homo | J AC | ACCOSTOR DUMAN | ACT 08731 HOWO | 4 AL391314 | 6 AL160176 Human | 9 AC074339 Homo | 8 AC144998 Pan t | 0 AC008130 Homo | 0 AC098800 Homo | 1 AC005391 Homo | 1 AC108471 Homo | 3 AC022023 Homo | 6 AC012146 Homo | 5259 AC025259 | 4 AC006084 Homo |
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6295. .6403,6639. .6735,6933. .7032,7372. .7478,7596. .7745,
7977. .3977,8365. .8487,9061. .9276,12298. .12428,
12534. .12570)
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6295. .6403,6639. .6735,6933. .7032,7372. .7478,7596. .7745,
7876. .7977,8365. .8487,9061. .9276,12298. .12428,
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KNITLKEHKLWUYTHERLKTINLOGLINNBIPDCYTFSVLITFDNKAHSGRIPISLE
TQAHIQECKHPSVPQHGDNSFRLLFDVVVILTGSLEFLCARSLLRGFLLQNEFVGFN
WRQRGRYISLWARLEFVNGWYILLVTSDVLITSGTILKGTSLRANLASYDVGSILLGF
STLLVWVGVIRYLTFFHNYNILLATLRVALPSVMRFCCCVAVIYLGYCFCGWIVLGPY
VLKRELSMVSBCLFSLINGDDMFVTFPAMQAQGRSSLVWLFSQLSYSFISLFIYM
VLSLEFLITGAYDTIKHPGGAGEESBLQAXIAQCOSPTSGKFRRGSGSACSLLCC
CGRDPSEEHSLLVN
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lkyffmspcdkfrakgrkpcklmlqvvkilvvyvglilfglsnglavyfpreentiafr
Hlfilgysdgaddtfaaytreglygaifhavdgylalpdvslgryayvrgggdpwtng
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                                                                                                              Direct Submission
Submitted (13-JUL-2000) Molecular Neurogenetics, Harvard Institu
of Human Genetics, 77 Ave. Louis Pasteur, HIM Building Room 422,
Boston, MA 02115, USA
Location/Qualifiers
 gene encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTGGGCCCGGTATGCCGTGTCCGTGGGGGTGACCCTTGGACCAATGGCTCAGGGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCTCTCTGCCAGCGGTACTACCACCGAGGCCACGTGGACCCGGGCCAACGACACTTTGAC
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Mucolipidosis type IV is caused by mutations in a movel transient receptor potential channel Hum. Mol. Genet. 9 (17), 2471-2478 (2000) 20489419
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| (人) 191 ほかいかん あいかいかん かんかん かんかん かんりょう | 140 | | Db 140829 ATTGATCCGATGGTTACTGGTGAGT | • | DD 140889 AGCIGCIGGGAITPAAAICAACAGCTGT Qy . 301 AGCACTTTGGGAGGCTGAGGAGGAAGGAAGGAAGGAAGGA | Db 141009 GGCCACGTAGGAAGACCTTGTCTCTACG Oy 421 CCCTGTGGTCCCAGCTACGAGGGGG | 141069 | 141 | Cy 541 CTGTCTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA | Oy 601 GCCACGTAGAAAGCACCAGATGTTATAT | . 661 | 141309 | Oy 721 GCCACTGGGGACTCTGGGGAGACCAGCC | Qy 781 ACTCCCTGTCCTTAGACTGCATCCAGGT | Qy 841 GCGACGATCTCACCCTCTTGGAAAGCAG | 901 | OY 961 TCTCACCCAGCAACTACTTCCCTAAGG | 1021 | 1081 . 141729 | Qy 1141 CTGGTCANTGTCACCATCCACTTCCGGC |
|---|-----|---|-------------------------------------|-------------|--|---|---|--|---|--|--|---|---|-------------------------------------|--|--|------------------------------------|--|---|--|
| 6880 CCTTGGGGCTGCCAAGGTTTACTCTGCCCCAAGACCCCAAAAAAAA | 150 | 6940 TTGACAACAAAGCACACAGGGGGGGATCCCCATCAGCCTGGACACCCAGGCCCACATCC 6999 | ⋖ | 7000 A 7000 | £ | හි | Mammalia; Eutheria; Primates; 1 (bases 1 to 173126) DOE Joint Genome Institute and Direct Submission | L Unpublished 2 (Dases 1 to 173126) 5 DOE Joint Genome Institute. | Direct Submission L Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA | S DOE Joint Genome Institute and Stanford Human Genome Center. Direct Submission L Submitted (01-JUN-2002) DOE Joint Genome Institute, 2800 Mitchell | Drive, Walnut Creek, CA 94598, USA E 4 (bases I to 17312) S DOE Joint Genome Institute and Stanford Human Genome Center. | Direct Submission Submitted (1911-2002) DOE Joint Genome Institute, 2 | Orive, mainer creek, to 34239, USA On Jul 12, 2002 this sequence version replaced gi:21306637. Draft Sequence Produced by DOE Joint Genome Institute www.jgi.doe.gov | ä | NOTE: This insert is not the entire sequence of the clone. It is clipped at the overlap with AC119396. The number of bases overlapped is 20300. Location/Qualifiers | rce 1.173126 / 173126 / mol type="genomic DNa" / db Xref="taxon:9606" / db Xref="taxon:9 | 39968 | Ouery Match Best Local Similarity 100.0%; Pred. No. 0; Matches 1501; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | 1 GCCGGACTCACAGGCCCTCCCCTTCTCTGCCCACAGTACCTGGCCTTGCCTGACGTGTCA 60 | 61 CIGGGCCGGIATGCGTATGTCCGTGGGGGGGGGCCTTGGACCAATGGCTCAGGGCTT 120 |
| qq | ò | qq | δλ | d d | RESULT 2 AC008878 LOCUS DEFINITION ACCESSION VERSION KEYWORDS | SOURCE | REFERENCE AUTHORS TITLE | JOURNAL REFERENCE AUTHORS | TITLE JOURNAL REFERENCE | AUTHORS TITLE JOURNAL | REFERENCE AUTHORS | TITLE JOURNAL | COMMENT | | FEATURES | sourc | BASE COUNT ORIGIN | Query Best Match | Qy Db 1 | ·· 강 음 |

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This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
runs of N, but the exact sizes of the gaps are unknown.
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/note="assembly_name:Contig15"
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/note="assembly_name:Contig16"
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/note="assembly_name:Contig19"
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                                                                                                              141969 GCAAGCGTGCGGGTGATGAGGGAGGGAGCCCGGGGTCTGTCAGGCCACCTGTCATGTGGA 142028
                                                                                                                                                                                                                                                                                    142029 ccrrddadarriadadarracachadarriadacacacanachadachadarachada 142088
                                                                                                                                                                                                                                                                                                                                                           142089 TIGACAACAAAGCACACAGTGGGGGGATCCCCATCAGCCTGGAGACCCAGGCCCACATC 142148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens chromosome 19 clone RP11-492L14, WORKING DRAFT SEQUENCE, 20 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (14-JAN-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Jun 17, 2000 this sequence version replaced gi:7344405.
                                                                                                                                                                 1321 GCAAGCGTGCGGGTGATGAGGGAGGCGCGGGGTCTGTCAGGCCACCTGTCATGTGGA 1380
                                                                                                                                                                                                                                               1381 CCTTGGGGCTTGGGGCTGCCAAGGTTTACTCTGCCCCCAAACTGGCCCCCACAGATCACGT 1440
                                                                                                                                                                                                                                                                                                                                 1441 TTGACAACAAAAGCACACAGAGGGGGATCCCCATCAGCCTGGAGACCCAGACCCACATCC 1500
                                                                                 1261 GGCTCCTGAGTTCCAGGGCAGGGACCTGGTCAGGGAGTGTCTTGGGAGCACTGGCCAAGG 1320
  1201 AATGAGATCCCGGACTGCTATACCTTCAGCGTCCTGGTGAGGCCCCCGGGAACCCACAG 1260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 155645)
Waterston,R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOTE: This is a 'working draft' sequence. It currently consists of 20 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    arbitrary, Gaps between the contigs are represented as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequencing vector: M13; 82%
Sequencing vector: plasmid; 18%
Chemistry: Dye-primer ET 77% of reads
Chemistry: Dye-primer ET 77% of reads
Chemistry: Dye-terminator Big Dye; 23% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 145925 bases at least Q30
Consensus quality: 146521 bases at least Q30
Insert size: 167000; agarose-fp
Insert size: 167000; agarose-fp
Unality coverage: 3.76 in Q20 bases; sum-of-contigs
Quality coverage: 3.76 in Q20 bases; sum-of-contigs
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Center code: WUGSC
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HTG: HTGS PHASE1; HTGS_DRAFT.
HOMO Sapiens (human)
HOMO sapiens
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AC021153/c
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JOURNAL
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TITLE
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                                                                                                                                                                     CACTCGAGGGGGCCCAGGGTGGGGAGGCAGCACTAGGCAC 127443
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pin 1 (MCOLNI) gene, exons 6 and 7.
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                                                                                                                                                  CTIGGAAAGCAGCICCAGTIACAAGAACCICACGCICAAAIICC 900
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                                                                                             TGCATCCAGGTGGATCCCCCCGAGCGCCCCCTCCGCCCCCAA
                                                                                                                                                                                                                        CACTCGAGGGGGCCCAGGGTGGGGGAAGGCAGCACCACTAGGCAC
adadaccadecerecededecereadecerriceere
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 AACCCACAGGGCTCCTGAGTTCCAGGGCAGGGACCTGGTCAGGGAGTCTTGGGGAGCAC 300
                                                                                                                                                                                                                                                                                                                                                           Submitted (13-SEP-2000) Molecular Genetics, The Weizmann Institute of Science, P. O. Box 26, Rehovot 76100, Israel Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301 TGCCCAAGGCCAAGCGTGCGGGTGATGAGGGAGGGAGCCCGGGGTCTGTCAGGCCACCTG 360
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                                                                                                                                                                                                                             Bargal,R., Avidan,N., Ben-Asher,E., Olender,A., Zeigler,M.,
Frumkin,A., Raas-Rothschild,A., Glusman,G., Lancet,D. and Bach,G.
Direct Submission
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Identification of the gene causing mucolipidosis type IV
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Pred. No. 3e-115;
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
129. 225
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/gene="MCOLN1"
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/number=6
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PRI 09-NOV-2000

H5A293659 2272 bp mRNA linear PRI 05 HOMO sapiens mRNA for mucolipidin, short form (ML4 gene). AJ293659

alternative splicing, ML4 gene, mucolipidin. Homo sapiens (human)

AJ293659.1 GI:10045134

LOCUS DEFINITION ACCESSION

VERSION KEYWORDS SOURCE

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PMAQGILSASCTTTBATWTRPTTHLTLIRWWLLTASRWIPPSGPLRPPATISPSWKAA
PVTRTSRSWGTGPPRFRWCLLGEHFPC
QLQGQHVADDAGTWGRKGPBDAPDPHPSLLPRLVNVTHFRLKTINLOSLINNEIPDC
QLTGGAHVADGKGRGREN PRILETOAHIOECKHPSVPQHGDNSFRLLFUCKLINTESP
SFLLCARSLLRGFLLQNEFVGFWWRQRGRVISLWERLLEFVNGWYILLVTGSL
SFLLCARSLLRGFLLQNEFVGFWWRQRGRVISLWERLLEFVNGWYILLVTSDVLIISGT
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PCCCVAVIYLGYCFCGWIYLGPYHYKFRSLGMVSECLFSLINGDDMFVTFAAMGAQOG
RSSLWLFSQLYLYSFISLFIYMVLSLFIALITGAYDTIKHPGGAGAEESELQAYIAQ
CQDSPTSGKFRRGSACSLLCCCRAPPSEEHSLIVN"
748 C 647 9 455 t
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|protein_id="CACO7B13.1"
|db_xref="GI:L0045135"
|trānslation="MTPSQPTRGSSCTRPSSMLWTSTWRCLTCHWAGMRMSVVGVTLG
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                                                                                                                                                                                                                                                                                                                                                                            Borsani G., Telethon Institute of Genetics via Olgettina 58, 20132 Milano, ITALY
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                                                                                                                   Borsani, G. Cloning of the gene encoding a novel integral membrane protein, mucolipidin-and identification of the two major founder mutations causing mucolipidosis type IV
Am. I Hum. Genet. 67 (5), 1110-1120 (2000)
                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                             Bassi, M.T., Manzoni, M., Monti, E., Pizzo, M.T., Ballabio, A. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="alternative splicing, short form"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
/db_xref="taxon:9606"
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1. .2272
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/gene="ML4"
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Borsani, G.
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| Db 301 GAGGCACACTAGGCACTCTCACCCCAGCA 332 | RESULT 7 AF30557283 LOGINGARY PRI 26-DEC-2000 DEFINITION Homo sapiens mucolipin 1 (MCOLNI) gene, exons 3 and 4. ACCESSION AF305574:1 GI:11991200 | SECRECT SECRET SOURCE Homo sepiens (human) SURFERENCE Homo sepiens (human) REFERENCE Homo sepiens (human) REFERENCE Homo sepiens (human) REFERENCE NUTSE Homo sepiens (human) REFERENCE AUTHORS RETURNING HOME SECRETARY N. Ben-Saher E. Olender Z. Zeigler, M. Canalitation of the control of the | RESULT 8 AC020978/C LOCUS DEFINITION Homo sapiens chromosome 16 clone RP11-96D1, complete sequence. ACCESSION AC020978 ACCESSION AC020978.10 GI:28933544 KEYWORDS HTG. SOURCE Homo sapiens (human) ORGANISM Homo sapiens Charyota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; |
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| Db 951 GGGACCCGAAGACGCCCCTGACCCTCAAGCCTCCTGCCTAGGCTGATGTCAC 1010 | Qy 1155 CATCCACTTCCGGCTGAAGACCATTAACCTCCAGAGCTCAACAATAATGAGATCCCGGA 1214 Db 1011 CATCCACTTCCGGCTGAAGACCATTAACCTCCAGAGCCTCATCAATAATGAGATCCCGGA 1070 Qy 1215 CTGCTAATACCTTCAGCGTCCTGGTGAGGCCCCCGGGGAACCCACA 1259 Db 1011 CTGCTAATACCTTCAGCGTCCTGGTGAGGCCCCCGGGAACCCACA 1259 | שטשיבי האמש שאמש שאיייש האמש שאמש שייש שייש שייש שייש שייש שייש ש | Qy 822 CGGCCCCTCCGCCCCCAGCGACGATCTCACCCTCTTGGAAAGCAGCTCCAGTTACAAG 881 Db 181 CGGCCCCTCCGCCCCCCAGCGACGATCTCACCTCTTGGAAAGCAGCTCCAGTTACAAG 240 Qy 882 AACCTCACGCTCAAATTCCACAGTACTGCCTGCTCACTCGAGGGGGCCCAGGGTGGGG 941 Db 241 AACCTCACGCTCAAATTCCACAAGTACTGCCTGCTCACTCGAGGGGGGCCCAGGGTGGGG 300 Qy 942 GAGGCAGCACTCTAAATTCCACAAGTACTGCCTGCTCGAGGGGGGCCCCAGGGTGGGG 300 Qy 942 GAGGCAGCACTCTCAACTCTCACCCCAAGCA 973 |

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Submitted (31-DEC-2002) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA (Dases I to 16429)
DOE Joint Genome Institute, Stanford Human Genome Center and Los Alamos National Laboratory.

Direct Submission
Submitted (13-MAR-2003) DOE Joint Genome Institute, 2800 Mitchell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           254 AAAATCAACAGCTGTGGCTGGGCACGGTGGCTCACGCCTATAATACCAGCACTTTGGGAG 313
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                                                                                                                                                                                                       Submitted (12-JAN-2000) Production Sequencing Facility, DOB Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA 1 bases 1 to 164223) DOB Joint Genome Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (13-APR-2002) Production Sequencing Facility, DOE Joint denome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA 5 Loss 1 to 164283 DOE Joint Genome Institute.
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Submitted (06-FEB-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
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Draft Sequence Produced by DOB Joint Genome Institute
                                            DOE Joint Genome Institute, Stanford Human Genome Center and Los Alamos National Laboratory.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Estimated Total Number of Errors is 0.1.
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45748 a 40339 c 37698 g 40508 t
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/mol type="genomic DNA"
/db xref="taxon:9606"
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DOE Joint Genome Institute.
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                           (bases 1 to 164293)
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nes 282; Conservative
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64115 GCTATGATCACGCCACTGCACTCCAGCCTGGGTAACGGAGCAAGACCCTGTCTCCAAACA 64056
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  HTG 29-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rowen, L., Madan, A., Oin, S., Abbasi, N., Baradarani, L., Birditt, B., Bloom, S., Dors, M., Dickhoff, R., Fleetwood, P., Harrison, G., Kaur, A., Madan, A., Nesbitt, R., Shaffer, T. and Hood, L. Sequencing of human chromosome 15 D15S146-D15S117 region
494 GCTATGACCACGCTGCTGCACTCCGCGGGGGACAGAGTGAGAGCCCTGTCTCAAAAAA 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Bloom,S., Dors,M., Dickhoff,R., Fleetwood,P., Harrison,G.,
James,R., Kaur,A., Madan,A., Owen,M.P., Ratcliffe,A., Shaffer,T.
                                                                                                                                                                                                                                                                                                                                                                                                                                     AC022403

B9666 bp DNA linear HTG 29-JAN-2
Homo sapiens chromosome 15 clone CTD-2120M24 map 15g21, WORKING
DRAFT SEQUENCE, 19 ordered pieces.
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All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp.

Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.
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* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

* 6943 7042; gap of unknown length

* 7043 14998: contig of 7456 bp in length
* 1499 14598: gap of unknown length
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Sequencing vector: pUC18, 108752
Sequencing vector: pUC18, 108752
Chemistry: Dye-terminator Big Dye; 90% of reads
Chemistry: Dye-terminator Big Dye; 10% of reads
Chemistry: Dye-primer Big Dye; 10% of reads
Sasembly program: Phrap; version 0.990399
Insert size: 75000; agarose-fp
Quality coverage: 3.0x in Q20 bases; sum-of-contigs
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Center code: UWMSC
Web site: http://chroma.mbt.washington.edu/msg_www
Contact: leerowen@systemsbiology.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AC022403.4 GI:8189326
HTG; HTGS_PHASE2; HTGS_CANCELLED; HTGS_DRAFT.
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                                                                                                                                                                554 AAAAAAAAAAAAAAAA 571
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2 (bases 1 to 89666)
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PRI 09-JAN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genome Sequencing Center, Washington
dicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (26-AUG-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entire insert of this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.
                                                                                                                                                                                                   Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. 1 (bases 1 to 15521) Sulston,J.E. and Waterston,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOTICE: This sequence may not represent the entire insert of this folds. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 (bases 1 to 155521)
Waterston,R.H.
Direct Submission
Submitted (25-AUG-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Mo 63108, USA
5 (bases 1 to 155521)
Waterston,R.H.
                                                                            DNA linear PRI 09-JA
from 7, complete sequence.
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Center code: WUGSC
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Ozersky, P., Du, H. and Maupin, R.
The sequence of Homo sapiens BAC clone RP11-723C11
Thombblished (2001)
3 (bases 1 to 155521)
Waterston, R. H.
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Contact: sapiens@watson.wustl.edu
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                                                                                                                                                                                                                                                                      Toward a complete human genome seque
Genome Res. 8 (11), 1097-1108 (1998)
                                                                            155521 bp
BAC clone RP11-723C11
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Submitted (27-MAY-2000) Genome
University School of Medicine,
MO 63108, USA
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Waterston, R.
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                                                                                           Homo sapiens
AC069335
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KEYWORDS
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/note="This clone overlaps RPI1-127P14 and RPI1-526A8"
17023 c 16451 g 25684 t 1924 others
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Pred. No. 2.4e-46;
0; Mismatches 54; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                         62413: gap of unknown length
65883: contig of 3470 bp in length
65983: gap of unknown length
72930: contig of 6947 bp in length
74718: contig of 6947 bp in length
74718: contig of 1688 bp in length
76840: contig of 2022 bp in length
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of 3889 h
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of 1651 b
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of 2265 }
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of 1781 h
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/db_xref="taxon:9606"
/chromosome="15"
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/note="similar to Mus musculus EST AA667697 (NID:92626398)
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 /note="similar to Bos taurus EST AW660583 (NID:g7426410)"
                                                                                                                                                                                                                                        321. .4331
note="match to EST AW594046 (NID:g7281304) hg44a03.x1"
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hnote="similar to Homo sapiens EST BF978105
(NID:912345320)"
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7465. .7709
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8856. .7151
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rpt_family="AT_rich"
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4566. .4626
/rpt_family="ERV1"
4641. .4889
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646. .9768
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10063. .10391
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10396. .10669
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5495. .5522
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10190. .10215
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264. .7455
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8600. .8736
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9398. .9590
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/rpt_family="Alu"
1303. .4459
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1890. .5219
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                                                                                                               The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 511-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and Coworkers at the Roswell Park Cancer Institute
                                                                                                                                                                                                                                                                                                            The clone sequenced to the left is RP11-785H2; the clone sequenced to the right is RP4-592P3, 2000 bp overlap. Actual start of this clone is at base position 1 of RP11-723Cl1; actual end is at base position 46589 of RP4-592P3.
Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information boot the map position of this sequence, see http://www.nhgri.nih.gov/DIR/GHR7, send mailto:egreen@nhgri.nih.gov , or see http://genome.wustl.edu/gsc
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/note="match to EST BF327818 (NID:g11298566)"
3665. .3850
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Homo sapiens"
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3455. .3606
/rpt_family="MER1_type"
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/db_xref="taxon:9606"
/chromosome="7"
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2616. .2709
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/clone_lib="RPC1-11"
18. .264
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(838. 101)
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1017_.2417
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210. .1505
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418. .2549
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1508. .1818
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925. .2100
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193267 bp DNA linear HTG 08-SED-2001

Homo sapiens chromosome UNK clone RP11-795E24, *** SEQUENCING IN
PROGRESS ***, 50 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (07-SEP-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
                                                       482
                                                                                                                                     GGCTGCAGTAAGCTATGACCACGCTGCTGCACTCCACCCTGGGTGACAGAGTGAGACCCT 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 193267)
Waterston, R. H.
                                                CTGTGGTCCCAGCTACTCAGGAGGCTGAGGCAGGATCGCTTGAGTCCGGGAGGTTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOTE: This is a 'working draft' sequence. It currently consists of 50 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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gap of unknown length
contig of 1741 bp in length
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contig of 1293 bp in length
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contig of 1036 bp in length
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contig of 1602 b
gap of unknown l
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Center project name: H_NH0795B24
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AC093695.1 GI:15487543
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Waterston, R.H.
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Homo sapiens (human)
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15987:
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COMMENT

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79.1%; Pred. No. 3.8e-46;
tive 0; Mismatches 70; Indels
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Homo sapiens
                    Matches 265; Conservative
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1967 159066: gap of unknown length

1067 171696: contig of 12630 bp in length

10796: gap of unknown length

1979 183547: contig of 11751 bp in length

1648 183647: gap of unknown length

1648 193267: contig of 9620 bp in length.

10cation/Qualifiers
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/hote="assembly_name:Contig47"
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                                                                                                                                                                                                                                                                                                                                                                                 8665. .9957
/note="assembly_name:Contig31"
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/note="assembly_name:Contig33"
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/note="assembly_name:Contig39"
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/note="assembly_name:Contig40"
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58953. .61438
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                                                                                                                                                                                                                                            'note="assembly_name:Contig21"
                                                                                                                                                                                                                                                                                          190. .5968
/note="assembly_name:Contig28"
                                                                                                                                                                                                                                                                                                                                                    /529. .8564
/note="assembly_name:Contig30"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="assembly_name:Contig34"
|5988. .18056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="assembly_name:Contig35"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18157. .19426
/note="assembly_name:Contig36"
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/note="assembly_name:Contig37"
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                                                                                                                                                                                                                  'note="assembly_name:Contig19"
                                                                                                                                                                                                                                                                          'note="assembly_name:Contig25"
                                                                                                                                                                                                                                                                                                                                  note="assembly_name:Contig29"
                                                                                                                                                                                                                                                                                                                                                                                                                               'note="assembly_name:Contig32"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="assembly_name:Contig42"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note="assembly_name:Contig50"
                                                                                                                          organism≈"Homo sapiens"
                                                                                                                                        /wol_type="genomic_DNA"
/db_xref="taxon:9606"
                                                                                                                                                                       chromosome="UNK"
clone="RP11-795E24"
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                                                                                                                                   243 CTGCTGGGGATTAAAATCAACAGCTGTGGCTGGGCACGGTGGCTCACGCCTATAATACCAG 302
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Mammalia; Eutheria, Primates; Catarrhini, Hominidae, Homo
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Rowen, L., Madan, A., Qin, S., Baradarani, L., Birditt, B., Bloom, S.,
Buxke, J., Dors, M., Fleetwood, P., Kaur, A., Madan, A., Nesbitt, R.,
Pate, D. and Hood, L.
                                                                                                                                                                                                                                                                                                                                                                                           303 CACTITGGGAGGCTGAGGAGGAAGGATTGCTTGAGGCCAGAAGTTTGAGACCAGCCTGGG
      0; Gaps
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On Jun 23, 2001 this sequence version replaced gi:13489137.
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Contact: leerowen@systemsbiology.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        reads
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Chemistry: Dye-terminator Big Dye; 90% of re
Chemistry: Dye-primer Big Dye; 10% of reads
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                                                     Note: Data from overlapping BACs AC022403 [drafting center UWMSC], AC012170 [drafting center UWMSC], and AC012170 [drafting center UWMSC], and AC01770 [drafting center WIBR] was added for finishing. Location/Qualifiers
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                                                                                                                                                                                                                                                                   RP11-562A8,
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                                                                                                                                                                                                                                                                                       consensus
                                                                                                                                                                                                                             /clone="RPI1-120K9"
/clone lib="RPC1 human BAC library 11"
/clone lib="RPC1 human BAC grown of the consens
RPI1-507018, and RPI1-127P14 was added and the consens
sequence was determined from RPI1-120K9 to the extent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30143 GAGGTAGGAGGATTGCTTGAGCCTGGGAGGCAGAGTTTGCAGTAAGCCGTGTTTGTGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             389 CACAAACAAATTAGCTGGCGTGGCGTGCCCCTGTGGTCCCAGCTACTCAGGAGGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 83.0%; Pred. No. 7.6e-46;
Matches 253; Conservative 0; Mismatches 52; Indels 0; (

    28670
    /note="woerlap with RP11-562A8 AC012170"
    /note="woerlap with CTD-2120M24 AC022403"
    14970
    14970

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12890. 122895
1000="low quality data"
137064. 166138
/note="overlap with RP11-507J18 AC012100"
33203 c 32122 g 46740 t
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hote="worlap with RP11-127P14 AC017700"
83485. .83535 /
hote="low quality data"
/15380. .15420 /
/noce="low quality data"
/10000 121920
program: Phrap; version 0.990399
                                                                                                                                          organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                           /note="low quality data"
13360. .43370
                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note="low quality data"
                                                                                                                                                             /mol_type="genomic_DNA"
/db_xref="taxon:9606"
/chromosome="15"
                                                                                                                                                                                                                map="15q21.2"
                                                                                                                            . .166138
                                                                                                                                                                                                                                                                                                                        possible"
Assembly
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RESULT 13 AC007501/c

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PRI 28-JAN-2000
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[bases 1 to 162617]

Bruce, D., Mundt, M., Doggett, N., Munk, C., Saunders, E., Robinson, D., Jones, M., Buckingham, J., Chasteen, L., Thompson, S., Goodwin, L., Bryant, J., Tesmer, J., Meincke, L., Longmire, J., White, S., Tatum, O., Campbell, C., Fawcett, J., Maltbie, M., Bussod, M., Sutherland, R., Sequencing of Avena Chromosome 16q12

Uppublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bruce, D., Mundt, M., Doggett, N., Munk, C., Saunders, E., Robinson, D., Jones, M., Buckingham, J., Chasteen, L., Thompson, S., Goodwin, L., Bryant, J., Tesmer, J., Meincke, L., Longmire, J., White, S., Tatum, O., Campbell, C., Fawcett, J., Malbie, M., Bussod, M., Sutherland, R., McMurry, K., Han, C. and Deaven, L.

Direct Submission

Submitted (06-MAY-1999) Center for Human Genome Studies, DOE Joint Genome Institute, Los Alamos National Laboratory, MS M888, Los Alamos, NM 87545, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (28-JAN-2000) Center for Human Genome Studies, DOE Joint Genome Institute, Los Alamos National Laboratory, MS M888, Los Alamos, MR 87545, USA
On Jan 28, 2000 this sequence version replaced gi:4755165.
Location/Qualifiers
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Bruce, D., Mundt, M., Doggett, N., Munk, C., Saunders, E., Robinson, D., Jones, M., Buckingham, J., Chasteen, L., Thompson, S., Goodwin, L., Cargaryatt, J., Tesmer, J., Meincke, L., Longmire, J., White, S., Tatum, O., Campbell, C., Fawcett, J., Maltbie, M., Bussod, M., Sutherland, R., Direct Submission
AC007501 162617 bp DNA linear PRI 28-JAN-200
Homo sapiens chromosome 16 clone RPCI-11_67113, complete sequence.
AC007501
                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Large Scale Sequence Analysis and Annotation with the Sequence Comparison Analysis (SCAN) System
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/chromosome="16"
/clone="RPCI-11_67113"
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9319. .9424
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/rpt_family="HSATI"
complement(9975. .10
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9067. .9178
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13723. 14353
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15420. 15715
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2600. .8727
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complement(9295.
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3933. .4186
                                                                                        AC007501.2 GI:6806839
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Homo sapiens
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30256. 30352
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complement(21897. .21993)
/note="RRAIL 2 excellent exon, frame
24603. .24673
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/rpt_family="MST"
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complement (51042. .51159)
/rpt_family="Alu"
complement (5349. .53495)
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57045. .57361
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/rpt_family="MLT"
29445. 29512
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29868. 29940
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complement(57046. .s
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9163. .29644
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                                                                                                                                                                                                                                                                                                                                                                                                                               /note="GRAIL 2 excellent exon, frame 2"
complement (join(107828. 108100,108901. .109154,
113458. .113541,115201. .115353))
//mote="Homo sapiens CAGF9 mRNA, partial cds. (U80736)"
108755. .108820
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                296 ATACCAGCACTTTGGGAGGCTGAGGAAGGATTGCTTGAGGCCAGAAGTTTGAGACCA
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Best Local Similarity 73.4%; Pred. No. 2.2e-45;
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gap of contig gap of

100 bp of 725 bp in length 100 bp of 711 bp in length

contig of gap of 100

gap of

in length in length in length

100 bp of 709 bp 100 bp

contig of gap of contig of

gap of

100 bp of 704 bp

100 bp of 717 bp in length

gap of 100 contig of

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gap of 100 contig of contig of

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gap of 10 contig of

100 bp of 714 bp in length 100 bp of 694 bp in length

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                                                                  * NOTE: This record contains 74 individual
* sequencing reads that have not been assembled into
contigg. Runs of N are used too separate the reads
* and the order in which they appear is completely
* arbitrary. Low pass sequence sampling is useful
identifying clones that may be gene-rich and allows
overlap relationships among clones to be deduced.
* However it should not be assumed that this clone
* will be sequenced to completion. In the event that
the record is updated, the accession number will
* be preserved.
Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
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10324 CGGTGGCTCACACCTGTAATCCCAGCACTTTGGGAGGCTGAAGGGGGAAGATGGCTTGAG 10383
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14.6%; Score 219.2; DB 2; Length 59634;
Best Local Similarity 77.5%; Pred. No. 3.1e-45;
Matches 279; Conservative 0; Mismatches 78; Indels 3; Gaps
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Search completed: October 27, 2003, 15:41:41 Job time : 6024.64 secs